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| Gene Name | Coriell DNA Panel(s) | Amplicon No. | Amplicon No. Total SNPs Missense Silent | lissense | Silent | UIR | UTR Intronic |
|--|-----------------------------|--------------|---|----------|--------|-------------------|--------------|
| | | | | | | | |
| Aminopeptidase P (XPNPEP2) | 24 + 47 (55AA) + 12pt | 24 | 30 | 0 | 7 | 7 | 21 |
| Bradykinin B1 receptor (BDKRB1) | 24+ 95 (8AA, 103 CAU) +12pt | 7 | 14 | 7 | 5 | ب ا | 4 |
| Bradykinin B2 receptor (BDKRB2) | 24 (8AA) +12pt | 12 | 36 | 8 | 7 | 14 | 17 |
| NK1 tachykinin receptor (TACR1) | 24 (8AA) +12pt | 7 | 6 | 0 | 3 | 6 | m |
| C1 esterase inhibitor (C1NH) | 24 (8AA) +12pt | 10 | 9 | 7 | 7 | 0 | 7 |
| Kallikrein 1 (KLK1) | 7 (7AA) +12pt | ς. | 9 | _ | - | 7 | 7 |
| Protease Inhibitor 4 (PI4) | 7 (7AA) +12pt | ∞ | 12 | _ | c | 1 | 7 |
| Angiotensin Converting Enzyme 2 (ACE2) 7 (7AA) +12pt | E2) 7 (7AA) +12pt | 20 | 6 | 0 | 0 | 0 | 6 |
| Totals: | | | 122 | 6 | 81 | 30 | 8 |

| | CDNA_SEQ_ID CDNA_SEQ_POS | 2085 | | | | | | | | | | | | | T | | | T | Ī | | | | 8 | 129 | | | | | | | | | | ١ | ١ | ١ | 1 | 3608 | l | | | | 543 | | | 1 | 200 | L | | | 1278 | 22, | 907 | 285 | | 894 | | | | Ş | 223 | 705 | | \$ | | | | L | ğ | Ш |
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| | WA. SEQ. ID | U90724.1 | | | | | | | | | | | | | Ī | T | I | | | | | | DA_000710.1 | NM 000710.1 | | | | | | | | | | , 000000 | 000000 | M 000003 | M 00003 1 | NM COOK23 1 | IM 000623.1 | 0A 000623.1 | | | DA 001058.2 | NM 0010582 | | | NAV 001058.2 | AL 0010582 | THE COLORS | | (M 000082.1 | (M 000062.1 | A 00002.1 | NM 002257 1 | | MM 002257.1 | | | | 000/10 | NM 000710.1 | M 000710.1 | | NM 000623.1 | | | | M common 1 | MM 000623.1 | M 000623.1 |
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| | ĕ | 200 | | | | l | | | | ŀ | | + | 1 | 1 | 1 | 1 | | | t | - | - | İ | 880 | 8 | | 1 | 1 | 1 | 1 | | | | | | | Ì | t | İ | | | | - | E | ATC | | | 1 | 82, | 3 | t | AGC | ШΒ | S E | 3 | | GAG | | 1 | | 2 5 | CTG | awe | | cat | † | 1 | 1 | 1 | 980 | |
| | REVCOMP RE | ŀ | - | ٥ | • | • | | | 0 | ۰ | | • | • | • | • | • | • | | | | | | | ٥ | ۰ | 0 | • | - | - | - | - | - | - | - | - | | - | ╬ | - | - | - | - | - | - | - | - | - | + | - | | • | - | • | - | - | • | • | • | • | 1 | , , | | - | - | | + | + | | - | - |
| | MUTATION TYPE RI | Sllent | Non-CDS | Non-CDS | Non-COS | 200 | Mon-Chs | Mon-CDS | Non-CDS | Non-CDS | Non-CDS | Non-CDS | Non-CDS | Non-CDS Non-CDS | Non-CD8 | Non-CDS | STOLENS : | 200 | TO COL | Non-Chie | Non-CD8 | Non-CDS | Massecite | Silent | Non-CDS | SQU-CD8 | SO 40 | Non-CDS | 20-02 | NON-CDS | Man-CDS | SOCIE | SOU | 800 | NON-COS | 200 | Manchia | 200 | 300 | Non-CD8 | Mon-CDS | Non-CDS | Sterr | Sterit | Non-CDS | Non-CDS | Non-CD3 | Non-Con- | Man Chic | Non-CDS | Silent | Misseriae | Maseriae | Misserse | Non-COS | Missense | Non-CD3 | Non-CDS | Non-CDS | | - Posterior | Silent | Non-CDS | Missense | Non-CDS | SCO COS | NOT COM | 211 | Masense | Non-CD8 |
| | EXON MU | Exon20 | Intron3 | Intron 15 | ┙ | Luciu. | Primory. | ot octifie | Intron 10 | Intron7 | El nota | Infrom 1.9 | Intron13 | Exon1 | Exon 1 | Phone: | mtron17 | /Luoni | C LODIE | Ewwo) | Fron21 | Fron21 | Exore | Exon2 | Exon3 | Exon1 | Exon3 | I foot | Inton. | intom! | i togu | Inton 1 | Ittou1 | nton2 | Exon3 | 2 | Exons | 2 5 | 2 0000 | From3 | S Plant | 3' Partic | Exon1 | Exort2 | Emortal 8 | ExonS | Exons | 200 | | Principal | Exon7 | Exon3 | E COURT | 2 20 | Stotl | Exon3 | Intron3 | 3' Flank | S lark | 200 | 2 200 | Emond | Intron1 o | Erong | SPark | 6Pank | Shark | N Comment | Frond | Exon3 |
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| | REF_SEQ_ID | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL CORECT 4 | Al 023653 1 | AL023853 1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | AL023653.1 | A.023653.1 | ALCZ SESS. | Al moses a | AI CORRES I | AI CORNERS 1 | 11482311 | 048231.1 | U48231.1 | U48231.1 | U48231.1 | ALS55102.2 | AL3551022 | Al 355102.2 | AL365102.2 | AL355102.2 | AL365102.2 | AL3651022 | A1365102.2 | AL355102.2 | A.300102.2 | ALJOSE CON S | A 1966100 0 | A1 955 170 2 | Al 365102.2 | AL365102.2 | AC007681.3 | AC007681.9 | AC007400.8 | AC007400.8 | AC007400.8 | A0007400.3 | AC007400.3 | XSAAM 1 | X54486.1 | X54486.1 | X54486.1 | AP277050 1 | AP277060.1 | AF277050.1 | AFZ77060.1 | AF277050.1 | AP277050.1 | 200 | 146911 | 116281 | AL366102.2 | ALSS5102.2 | AL356102.2 | AL965102.2 | AL356102.2 | A 200102.2 | A 965102 2 | ALS65102.2 |
| Table IV (1 of 2) | FLANK, SEQ REF (SEQ ID NO:) FLANK, SEQ ALT (SEQ ID NO:) | 001 | 101 | 201 | 103 | 10 | 3 5 | 605 | 60 | 901 | 110 | 101 | 112 | 113 | 114 | 116 | 116 | 117 | 118 | 8. | 200 | 138 | 12 | 124 | 125 | £ | 127 | 123 | 129 | 130 | 131 | <u>8</u> 1 | 133 | 2 | 38 | R | /8/ | RS | 8 | | 9 | 2 | 3 | 145 | 146 | 147 | 148 | 143 | 82 | 8 | 18 | \$ | 551 | 8 2 | 2 | 25. | 160 | . 191 | 22 | 611 | 210 | 614 | 616 | 616 | 617 | 618 | 619 | 8 | 200 | 623 |
| | FLANC, SEO REF (SEO ID NO: | - 37 | 8 | | | | | | | | | 48 | | | | | | | 8 | | | | | | | 83 | 2 | 99 | 8 | 67 | 8 | 8 | ę | 7 | 22 | P | , | e s | 21 | * | 2 | 8 | | 28 | 83 | . 64 | 28 | 8 | 49 | 8 8 | 8 | 16 | 82 | 8 3 | 8 8 | 8 | 2.5 | 8 | 8 | 220 | 200 | 285 | 583 | 584 | 989 | 983 | 28 | 1000 | 8 8 | . |
| | (REF / ALT) | | AGTGTTACA | TOCOCCAAG | CCAABCTBA | CCCTCACTC | 2000 0000 | ACATTER ACA | TTCGTGGC | TOAGTCACC | CTCCACCA | CAAGGCC | CAGGGTTAG | стстост | GOCTCGAGC | CTGATCTG | ACATA | таасттт | GGAGGAG | MANAGOCIG | TOOOCT | GGGGGGGG | ACTUAL OF | AT ITALY PROPAGEACT | TIC GATAAGAAA | ACCCTGTCT | GCCTATAAT | al accacacc | CCGCGCCCA | TOCCCTCT | стававатас | TGGGGACAG | CAGCACAGT | 1 occoctact | статосста | ПАСВСАВ | Iggerecer | CACAGGACA | CAGAIGI | ATTOUT OF | TROCTAR | AACCTGGGG | CCATCOCC | ATGACACAG | DOCCTROT | TTGGGAAAA | CAGCATGA | AGTGTGAGG | аладатата | TOCATOTOT | ICTI CAGGATATG | GAACCCAT | AATGAAGAA | CAT ACTOREGE | OCCTTOOL S | AGGAACCCG | GTCCAAGGG | TGACACAGC | овталтовс | 30GTCAT | GOTOCTO | AGGTCAGA | TESTATT | GAGGACT | AAGAGAAC | оссидам | FACAAAGAA | ACCCAGCC | SOCIECTO | CAGGAGAAC TIC GCCATCCAG |
| | 2 | Įš | TC TIC | 200 | CAG [T/C] | WO V | | 3 2 | 2 5 | No. | Ę | 5 | at low | (arc) | XT [MG] | AA ICYI G | A IMCI G | 30c T/01c | E . | BW S | 200 | 3 5 | 2 2 | | MT ITO | (O) | CA [[X | 3 | <u>⊰</u> 8 | è | οο | OCT GAN | Maj | 8 | 8 | 1 | 5 | | | | | | | | | | | | | | | | W CG | | 2 2 | A00 | CTG ICT | MGA ICIT | 150 150 | NATIO O | 2 C C C C | GA IGAN G | ATG ICAL | TT ICAN OT | TTC [C/A] G | CCG [CJ] | 00C (G/M | | AAG FA/A | AAC TICE (|
| | DS FLANK | астатс | AGAACA | CTCACC | AGGCCT | 8 | 3 | | E | AGCATO | AGGT | SCTCC. | GACCCA | TTCCCC | ЭССПТ | MATATT | GAAAGG | AGGATT | TGGAGG | | 315 | TATE OF | TOTOT | ATAAATG | ACAMAGA | ACGGAC | CAGTGG | GGCTCCC | 880 | A001C | GGGATG | aracra | AGGAC | atoccA | GCACA. | 194990 | AGGTGC | GAGIC | 5 5 | | TAAACA | CCATOC | CAACT | CAGGAC | TCTGC | GAATGG | TTTGAG | TOCAAG | OTCCAG | TOTO | 8 | TOCTATE | DE C | 1000 | 14000 | Tecco | GGACTC | GGCATG | 130 × | TOTCAT | 300 | ACOCO | TGGAG | Татста | SCTTCC | AAACAC | GTACG | ATGACA | 300 | CAGGAC |
| | CONTIG PO | Ē | 3 | | | - 1 | - 1 | | | - | | | | | | | 88 | ž | 8 | 8 | 9 | 2 9 | 8 | 1 | 8 | 136 | 240 | 98 | 22 | â | 242 | 253 | 717 | 89 | 82 | 8 | 20 | 2 | 8 | 3 5 | 9 | Ē | į | 200 | 9/9 | 25 | 8 2 | 317 | 5 | 2 | 8 | 985 | 9 | 5 | 3 8 | 8 | 111 | ğ | 2 | 6 | 2 | 2 | æ | 8 | 27. | 9 | ŝ | 8 | 900 | ŝ |
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| | 0 08 | - | AE10092 | 10083 | 10001 | 10085 | 8 | è | 9 6 | 9 | AF100s11 | 100s12 | AE100s13 | 100014 | 100815 | 100818 | 100417 | 100818 | 60 | Tomas | 200 | 700 | 3 | 1000 | AE10383 | 10394 | 10385 | 10481 | 10462 | 10483 | 10484 | 10485 | E104s6 | AE104s7 | Bago | 889 | 000 | AE104811 | 7180 | | 1040 | 7190 | 1880 | AE106s2 | 10843 | E108s4 | E106s5 | 10686 | 70007 | 1000 | 10543 | E105s4 | 5055 | AE10588 | 20703 | 10783 | E10794 | E107s5 | E107s6 | 986 | /800 | E103mg | E104618 | E104s19 | E104e20 | E104621 | 104s22 | 10 623 | 10403 | AE104628 |
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| | GENE DESCRIPTION | Aminovanificasa P (mandona hound | Aminopeotidase P (membrane-bound | Aminopeotidase P (membrane-bound | Aminopeptidese P (membrane-bound, | Ammopeptidese P (membrane-bound | Aminopeptidese P (membrane-bound | Amarchepasse P (memorana-count | Aminopological P. (mamorana-counc | Ambroadities P (membras bound | Aminopeolitiese P (membrane-bound | Aminopeptidese P (membrane-bound | Aminopeptidase P (membrane-bound | Aminopeptidase P (membrane-bound | Aminopepticase P (membrane-bound) | Aminopeptidase P (membrane-bound) | Aminopepticase P (membrane-bound | Aminopeptidase P (memorane-bound | Aminopeptidase P (membrane-bound | Aminopepagese P (membrane-bound | Ammobapacase P (membrane-count | Ammopelacese P (memorane-counc | Standard December 19 | Brachathin December 81 | Brachtania Receptor B1 | Brackfrith Receptor B1 | Bradykinin Receptor B1 | Bradydnin Receptor B2 | Bradykinin Receptor B2 | Bradykinth Receptor B2 | Bradytirin Receptor B2 | Bradytinin Receptor B2 | Bradykinin Receptor B2 | Bradykhih Recaptor B2 | Brachkinin Receptor BZ | Bradydmin Receptor B2 | Brackfortin Receptor B2 | Brackfurth Receptor B2 | Stadyorm Heospor B2 | Brackfells December Do | Brothfrin Boomhy R2 | Brackfrin Recentor B2 | Techyldrin Receptor 1 | Tachyldnin Receptor 1 | Tachyldrin Receptor 1 | Techyldrin Receptor 1 | Tachyldnin Receptor 1 | Tachyldrain Receptor 1 | Tachyidnin Receptor 1 | C1 Estates Inflored | C1 Esterate Introduc | C1 Esterase triribitor | C1 Esterase Inhibitor | C1 Esterese Inhibitor | Kathrain 1 (renal/morrane/makers/ | Kalitorin 1 (renal/pencrees/saffvary) | Keillunin 1 (renal/pencrega/sellyany) | Kalitorin, 1 (renal/pencress/salivary) | Kelffirein 1 (renal/pencrees/bellvary) | Bradytim Receptor B1 | Braddin Bearing By | Brackfrin Receptor B1 | Brach/dnin, Receptor B2 | Bradykinin Receptor B2 | Brackfahln Receptor B2 | Brachstrin Receptor B2 | Bradydnin Pacaptor B2 | Bracydrin Hacaptor B2 | Brighton Hecepor B2 | Brachktnin Receptor 82 |

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| Brachforin Receptor B2 | BOKABZ | AE104s27 | • | 1826 | ANGTOGOAN ICAT GACTGGGCA | 595 | | AL365102.2 | 62878 | 9 | Exou | NO-CIN | - | 1 | | 100 000 00 00 00 00 00 00 00 00 00 00 00 | |
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| gotensin Converting Enzyme 2 | ACE2 | AE109s7 | 5 | 241 | Q | 106 | | AKINDON. I | 8 | 4 | Τ | 900 | | | T | - | |
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| - Indicate Philippe A | 74 | AF110s4 | - | 380 | COCACAAAC IT/AI GCTTCGG | | | 1.28101.1 | 77.20 | - | Intron2 | Mon-CDS | • | | 1 | | ŀ |
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| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s30 | ß | - 1 | CCCICCAGGAAGGAATCICG | Ē | Ī | 1000 | 9 | | | | | 9 | A 047 | MA 000710 1 | 862 |
| Bradyldnin Receptor B1 | BOKRB1 | AE103s10 | 7 | | ACAAGGTGC[AG]GGGGCCGCA | 990 | | 18231 | 1978 | 3 | Т | MINISTER SECTION | • | 3 | П | - | |
| Bradyldnin Receptor B1 | BOKRB1 | AE103s11 | 7 | | aragacccng/apprateac | 999 | | 115231.1 | ě | < | Т | 200 | 1 | | Ì | | l |
| adyldnin Receptor B1 | BOKRB1 | AE103s12 | 4 | 1808 | CTCAAGGGGTAGCAAGTGATC | 2992 | | U48231.1 | 3058 | - | G Exort3 | NON-CDS | • | | Ť | | |
| advidnin Receptor B1 | BDKR81 | AE103a13 | 4 | 1946 | ACAAGTATCJACGGGTAATGGC | 999 | | 18231.1 | 3163 | 9 | Exorts | NO-CUS | • | | 1 | + | |
| wchtorin Receptor B1 | BDKR81 | AE103814 | _ | 200 | I OCTOTOTATIVO TACACITICO | 699 | | U48231.1 | 3181 | - | Eron3 | 802-E08 | • | | | | 1 |
| adviction Receptor B2 | BOKSB2 | AE104830 | ~ | 901 | gttgtgagga/gttAAAggcA | 870. | | AL365102.2 | 1080 | o | ┪ | SQ COS | - | | ı | Land County | 3 |
| advictin Receptor B2 | BDICHBZ | AE104831 | | l | | 129 | | AL365102.2 | 68030 | - | G Erond | Missense | - | GAC | 300 | 000623.1 | |
| artiforin Receptor R2 | BOKRB2 | AE104432 | ŗ | | AACTGACCTIG/AJAGTACAGTG | 672 | | AL365102.2 | 66339 | 9 | Intron1 | 800 | - | | | 1 | |
| advitorin Receptor B2 | BOKRB2 | AE104833 | • | | CTGACCTGA(G/A)TACAGTGAA | 673 | | AL355102.2 | 68341 | | A Intron1 | SQ-QQ | - | | 1 | | 1 |
| achdonin Receptor R2 | BOKRB2 | AE104834 | • | l | TCTGCTCCATICGGAGCTATT | 92.9 | | AL355102.2 | 62872 | ٥ | Exon3 | SQ -CQS | - | | 2 | 1000 | 3 |
| Brachforin Recentor R2 | BDKRB2 | AE104a35 | • | 8 | ATTICIAGACACTCAGTGTC | 876 | | AL355102.2 | 62688 | 0 | Exon3 | Non-CDS | - | | ∄ ! | W 000623 | |
| adviction Receptor B2 | BOKRB2 | AE104s36 | • | 619 | | 979 | | AL366102.2 | 62943 | 0 | A Eron3 | Non-CD8 | - | - | ı | 12000 | |
| change inhibitor 4 | Z | AE110810 | 2 | 397 | | 2119 | | 1.28101.1 | 9169 | o | G Exon4 | Steri | • | 8 | ¥ Sov | 006216.1 | 2 |
| visesa tritilitire A | 710 | AF110a11 | ļ | ğ | CACGGAAGITGTTTCC | 679 | | 1.28101.1 | 3612 | ပ | T Erront | Wissense | • | 8 | ١ | 006215.1 | 7 |
| viscon highline 4 | 76 | AF110a12 | ŀ | 200 | GGTACCGGATTTCATAA | 879 | | 28101.1 | 2524 | ٥ | T S' Rank | Non-CD8 | • | | 1 | 1 | |
| Tachyddin Becenter 1 | TACR | AE106s8 | 2 | 8 | ATGTAGATIAGIGTCTTGTGG | 988 | 1 | AC007400.3 | 141073 | 0 | A IntronA | Non-CDS | - | | + | | |
| Tardwidgin Bacandor 1 | TACR | AE10649 | | 8 | CCAGATAGIGCAGCTAG | 198 | | 10007400.3 | 143385 | ٥ | A Intron3 | Non-CD8 | - | | 1 | | l |
| Andotemen Converting Enzyme 2 | ACEZ | AE109s8 | 2 | 958 | | 682 | | AC003669.1 | 69475 | • | T Introv13 | Non-cos | - | 1 | | 1 | |
| | | | | | | - | | · company | ecase. | | T | Š | - | - | - | - | |

| The property lives | | | ļ | | | | | | | | | | | _ | _ | | |
|--|-----------|----------|-----|------------|-----|---|----------|------------|--------------|---------|--------|------------|-----------|---|---------------|------------------|--------------|
| Aminoperiodese P (membrane-bound) | XPMPEP | A£100s1 | - | E | ٥ | SATSTEASCCTSCTSTCTCGCOSASCATSTSASTSCCCTCA | 160 | 82 | AL023653.1 | 8882 | 9 | Exorego | Sam | + | 3 | 000 | e e |
| Aminopepitines P (membrane-bound) | XPNPEP2 | AE10042 | - | 82 | Y. | @TCTCCTTTBCAGAACAGTCCTJAGTGTTACACTGAGTCCAGT | 791 | ZZ. | ALGENESS.1 | 60150 | 7 | Short | Mon-CD8 | • | 1 | | - |
| Aminopepidase P (membrane-bound) | XPNPEPZ | AE10063 | - | ā | \$ | сслалттосостслосиситетесосслававаемоста | 168 | 82 | AL CORESA 1 | 74483 | ٥ - | 7 | Mon-CDS | • | + | + | + |
| Aninopepiidase P (membrane-bound) | XPNPEP2 | AE10084 | _ | ž | - | GGCCACTGACAAGGCCTCAGCTTCCAAGCTGAGCCTCATCCTA | 166 | £ | ALIEZSES3.1 | 74051 | - - | Preparits | Kan-CD3 | • | 1 | 1 | 1 |
| Animopepidase P (membrane-bound) | XPNPEPZ | AE100m5 | - | 8 | | АВАААВОВТТВВАВПВАВВВТАСТВВВВОССВАВТСТСТТТТ | 291 | 022 | ALCC2053,1 | 24540 | 7 | mean | Non-CD8 | • | + | + | + |
| Aminopeoliciese P (memorare-bound) | XPNPEP2 | AE100#6 | 1 | 2 | - | AGCACTECCCAGGCCACCCTCTTTATTATACCCTCTATG | 191 | ä | ALCC2053.1 | 78621 | 3 | trebon7 | Apr-CDS | 4 | \dagger | + | + |
| Aminopepidase P (membrane-bound) | XPIOTEP2 | | ۽ ۽ | ē ! | * | TTTGTTTGAGGAAAGGGTTTCTJGCTGCTTTTAAGAGGATGC | 691 | 22 | AL023653.1 | 9999 | ٠, | /water | SCO-CDS | • | 1 | + | 1 |
| Ammapagacana P (mentorana-bound) | YONGCO | | | S 8 | | TABLESCHITCHOLOGICAL AND CONTROL OF THE CONTROL OF T | g e | E i | ALCONO. | 98299 | 4 . | o i | S S | | \dagger | l | |
| Arricogolitase P (mentrane-trans) | XPMPEP2 | AF100m10 | 2 | 1 | - | TTOCAAACCTTAACATOCACCONTAAATCACCTTAAACCTTA | | \$ 8 | AL POTONS 1 | 00000 | - 0 | framen? | Man Che | - | \mid | | - |
| American P (mentions) | XPMPEPS | AEIMMI | : | 9 | | Ossocration and Company of the Compa | 6 | | 11 00000 | | , | t | 200 | • | | - | |
| Amiropanistan P (manbrana-brund) | XPMPEP2 | AF100m12 | : | 2 | | Anococcananations | 200 | | Al rezers : | 2004 | 1 | Ì | 3 5 | , | l | <u> </u> | - |
| Aminoanidase P (manipana-bound) | X DAME DO | AF10013 | * | | | pacetrocarda and particular and part | i f | 2 2 | 11 (2000) | 1 | , | 2 0 | 200 | , | ŀ | | - |
| Antinopolities P (membrane-bound) | XPNPEP2 | AE100#14 | - | Ā | \$ | GGAAAGGCCTTAAAGAAGAAGHCTCTTAAGAAAAAAAAACTTTTTTTTTT | 5 | . 8 | 1 130000 17 | 5 | | Front | Monechis | | | | - |
| Aminoperticiese P (membrane-bound) | XPMPEP2 | AE100e15 | - | 2 | | ACCTOTATOTOCTOCAGOOOTAAAAAAAAAAAAAAAAAAA | 5 | 92 | AL COMMENT | ş | ╀ | + | Man CDS | | - | | |
| Animopepidase P (membrane-bound) | | AErobere | 2 | ŝ | | CTTBCCTCAGGCAGATCAGCAAGTTAAATATTCCTTGTCAATT | 12 | 58 | AL DOTAGES 1 | 700 | 1 | ı | Man CD8 | | _ | - | _ |
| Aminopeolities P (membrane-bound) | | AE100s17 | z | 8 | | ACTEATACCATETTTATETTETTETTCTTTCTAGGGCCAGTGGG | Ę | 2 | ALGZ283.1 | 17.08 | - | Thom! | P | • | | | |
| Animopapitosee P (membrane-bound) | XPNPEPZ | AEtoosta | 2 | 8 | | MANTANTANAGCCAGIACISCCATCTGGTGTGTGCCAG | 8 | 20 | AL 027853.1 | 202 | 4 | 1 | MON-CDS | | | | |
| Animopepitidese P (membrane-bound) | XPNPEP2 | AE100e19 | 8 | 52 | | CTCCTCTGGCTCCTCCCGGATTCCTCCATATCACCTCTTCC | = | 34 | ALC23653.1 | 8895 | 0 | Present S | Mon-CD8 | • | | | |
| Aminopepitose P (membrane-bound) | XPNPEP2 | AE100s20 | u | 8 | ۰ | ACCICITIBACATIBACITIA/GRAAGACIBICACCCCTICI | žį. | 245 | AL023653.1 | 63469 | Α 6 | Properties | Non-CD8 | ۰ | L | | |
| Aninopeolichee P (membrane-bound) | XPHPEP2 | | æ | \$ | \$ | CCTATGGAGAAGGTCCCAGGIC/ADDCAGGAACACAGGGGCTTCT | 163 | 246 | AL023653.1 | 63628 | ٥ | Exorg1 | Mon-CD8 | ۰ | _ | | |
| Anticoecities P (menticens-bound) | XONPEPZ | AE100422 | 81 | £ | • | COSSIGNATIVACIACIONALIAS SOCIA TA TOCCASSICO | 25 | 247 | ALCCOSS3.1 | 92005 | 9 | Emmer | MonCDS | 4 | 1 | | - |
| Antinopapidase P Imentinang-bound | XPNPEP2 | AE100423 | 88 | <u>\$</u> | | CAGATGAGCCAGCATTCCAGCTTCACCCTTCAGCAACA | 165 | 248 | ALOZOBS3.1 | 64565 | 9 | Enoug | Mon-CDS | + | + | 1 | 4 |
| Statement Heceptor B1 | BOXES: | AETOS | • | à | | AATTATGTCTTGTGGGGGGAGCTCTTCAGGACCAAGGTCT | # | 92 | U48231.1 | 2202 | 6 | De C | Moserne | • | + | T | \downarrow |
| Suchdish Berson Bi | BOX HO | AE10362 | ┥. | E 1 | - | CTBCTBCACAGAGTBCTBCCAGAAACATTTATCATCTCCATCTB | 181 | 92 i | 1102311 | 96 | 0 . | Enorg | E Same | - | 8 | CCA NM 000710.1 | 1.0 |
| Brachkrin Receder 81 | NOCH. | AFIRM | - | § § | - | TOTTOTTOTTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT | | ē i | U48231.1 | 8 | 4 | | NON-CUS | | + | + | \mid |
| Bradykanin Receptor B1 | 900 | AEICOM | • | 2 | - | ATACTACTACAATTAYACCTOATTACACCTCCCCCCCCCC | X | 8 | 1000 | 8 | | 5 | 200 | - | $\frac{1}{1}$ | <u> </u> | <u> </u> |
| Bradytsinin Receptor B2 | BOKHBZ | AE104s1 | £ | * | ¥. | CAAATCTGCAGGGCTCCCCCCCGAGCGCCCCAGGTGGGCCCCC | 102 | 2 | At 365 to2 2 | 80'08 | 9 0 | + | Menchi | - | - | ļ | |
| Stadylarin Recoptor 82 | BDKHB2 | AE10462 | 10 | 28 | ۰ | AATCT9CA999CTCCCCQA9TCC9CGCCCA99T969CCCCT | žį | 500 | AL365102.2 | 72786 | < | monu | Man-CD8 | - | _ | ļ | |
| Andylanin Receptor B2 | BOKHBS | AE10463 | ٥ | 8 | 0 | AAGGCTGGCTGAGGTCATGTTATTCCCCCTCTGAGACTCAGTT | 183 | 88 | AL355102.2 | 20880 | 1 | Infort | Non-CDS | - | | | |
| radykinin Receptor B2 | BDKABS | A£104#4 | ٩ | £ | | CAGGGAGAGCTGGGATTGAGGCTTCTGGGGTGCTGCCTGTGGGG | ğ | 222 | AL265102.2 | 20000 | 9 | Inform | Men-CD8 | + | + | + | + |
| Kadyktwin Plecaptor B2 | BOXHBX | AE104e5 | 2 | 8 | | TGAGGCCTGGGGTGCTGCCTGATTGGGACAGCACACACATGCTT | 105 | 92 | ALMSTOR 2 | 7,0000 | • | THE COL | Mon-COS | + | | | _ |
| Inchesia Receptor R2 | BOKBB | AF1047 | 2 ^ | 1 | ≨ - | | 8E 5 | £ : | AL255102.2 | 98026 | 9 , | Mon | Non C28 | + | + | + | + |
| Pracydainin Receptor B2 | BOKHBZ | AE104e8 | Ŀ | 6 | | GGGAACTGAGGCAGAGAGGGGTTGATTGAGGAATATTG | 182 | į | AL MERITO | 9000 | | N S | 200 | - | ł | 1 | |
| Indystrin Receptor B2 | BOKINGS | AE1046 | • | 8 | - | ТОССАВТИСВТСТВСВТААТИКАТВОСТСАСАТВТАСЯТА | 901 | æ | ALSS6102.2 | 80.23 | - | 8 | 80 | - | | Net 000623. | L |
| radykinin Ascaptor B2 | BDXHBZ | AE104e10 | - | Ď. | | Тамслаатвалледаласслилатвласисстистатассл | 88 | 263 | AL365102.2 | 62801 | P V | Exercise | Non-COS | - | | NAC 000623.1 | |
| addition Receptor B2 | BOXCHER | AE104611 | 1 | £ | ۰ | ATMCAGCICATTGAGTCTTTAGCACAGACAGATGTTCTTTA | 8 | ž | AL355102.2 | 2112 | 1 | - | SCO-coa | + | | NM 000623.1 | \dashv |
| rachloren Receptor Big | BOKHBZ | AE104612 | - | E . | | GCTCATTGAGTCTTTCACAGGTTACAGATGTTCTTTATCAGGG | 202 | 15 | ALX55102.2 | 81138 | • | Frond | Mon-CD8 | - | 1 | NM 000823.1 | 388 |
| radium Pecentra Br | BOXHER | AETONETS | 1 | E 1 | | AABABABTCTCABACCATCACCTGTGTGTGCTGAATGAC | 8 | 98 | AL965102.2 | 61280 | 0 | Emmi | Non-CD8 | + | + | MAC 0008 | 1 |
| merbelinin Bernester Ro | Bractor | AE10416 | • | 8 8 | \$ | GOGATGATAACACATTGC/TCATTCCTTTTCACACTCTTC | ž | 292 | AL385102.2 | 92280 | 7 | Boar | Moncos | + | + | NAV 000823 | 288 |
| Individual Receptor 62 | BOKING | AF104e17 | 1. | £ £ | - | Transatinaminassiminassiminassiminassim | 8 | 2 1 | AL355102.2 | 2000 | e ' | N I | grucos | - | | + | |
| echylanin Receptor 1 | TACH | AE108s1 | - | i | - | ACCARACTORNOCATION INCLINICATION OF TOTAL CONTINUES | 8 | ŧ. | A.359102.2 | TACAL . | | į | STORY I | + | | | 1 |
| achybrin Receptor 1 | TACRI | AE10842 | ~ | æ | \$ | AGCAGGAGGCAGGACCANGTATGACACAGATGACCACTTT | 102 | Ē | ACTION S | 9,50 | | 9 | į | - | + | ATA ME CONDERS | 2 2 |
| achybinin Recaptor 1 | TACRI | AE108c3 | - | g | | аватвааттатетасстативросстастсисствостт | 208 | m | AC007400.3 | 1048 |) P | 1 | Mar CD8 | - | ╀ | Т | L |
| achytrin Receptor 1 | TACRI | AE1084 | • | ā | • | сламтвалтамтваясттюттввалмастватосалс | 210 | 122 | AC007400.3 | 139028 | 2 | Н | Non-CD8 | - | | | |
| Schridnin Receptor 1 | IACH | AE100m5 | - | £ | | CASTBATTTBQTTTBAGTCAICANCAGCATBAGGGTGGCAAAG | 211 | 504 | A0007400.3 | 130000 | ٩ | Enong | Moncos | + | | NM 001058.2 | |
| activismin Receptor 1 | I V | AETONA | ٠, | = | w. | CTBACCCTTTTGCMGTCCCCTMGTGTGAGGGTGTTTCTGAT | 212 | 273 | 4007400.3 | 139163 | 0 | Enong | 800 may | + | + | Ť | 1 |
| C. Esterno Intiliter | 3 | AE+ORa+ | • | E 8 | | T) development to the transport of the t | 212 | 22 | AC007400.3 | 130367 | | ğ. | į | + | 2 | TCA NM 001058 2 | 2 |
| C1 Esterate Intibility | ¥ | AFIOSO | | 2 | | GOOGLAGACHTTTAGACACACTOTTAGACACACTTTAGACACACACACACACACACACACACA | 100 | | 1 | 8 | < ° | T I | 0 | | ł | + | - |
| C) Edergee (f) Ditor | E E | AE108eg | | × | • | COCATCAMOTOROGICATCAGGATATGCTCTCAATCAT | 3.5 | 6 | CS40M 1 | 196 | | Parent L | | - | 204 | AOT MAL COOKS | 5 |
| C1 Enterang 1170Nor | CUM | AE105e4 | - | 8 | | TATCTCCAAGATGCTATTCGTAAACCCATCCTGGAGGTTT | 22 | 98 | New . | S S | • | 1 | | | ł | T | L |
| C1 Esterase Inhibitor | Z. | AE105es | - | 6 | 0 | GCTCTACCACGCCTTCTCAGCOBATGAAGAAGGTGGAAGACCA | 210 | 182 | X54486.1 | 2000 | | E E | Meneral | | | ۲ | |
| 1 | CIME | AE105e6 | • | E | ¥¥. | Techecocttocttttqs/attectstedaccaccaccac | 210 | æ | X54486.1 | 18012 | ٩ | Exone | Misserse | 0 | \dashv | 1 | |
| ₹. | ă | AE107s1 | - | 2 | - | TOCTGOCTAATGATGAGTGGAAAAAGCCCACGTCCAGAAG | 82 | R | AF277050.1 | £ | ٥ | ě | Meere | - | * | GAA NM 002257.1 | 71 985 |
| Ecen ((analysic sealistiver) | 2 | AEIONE | ╣. | 8 3 | | CAGACTETETAGCCCAABGCGVARBGGATTGGGGACTCCTGCGTC | ž | ž | AF277060.1 | 122 | ٩ | Interns | Moncos | • | + | T | - |
| Afficient 1 (remaithement and address) | 200 | AE167M | | E F | | ASSETURITION TO THE CANCEL AND THE CONTROL OF THE CONTROL OF THE CANCEL | 8 1 | SE 1 | AF277090.1 | 25 | 9 0 | E S | Meserree | • | 949 | CAG NW 002557. | \$ |
| California I (renal/banches/halharn) | S S | AF-107-6 | 1 | 8 | | OCCUPANT CONTROL COLORO IN COMPANDA CONTROL | S i | 8 1 | AFZT7060.1 | | ٦ | S C | Man CO8 | | + | | + |
| California I (renal/perches/suffvery) | 1 | AE107ed | | 188 | | Tercacerrocarcacercacerrocacereres | 5 8 | 2 | APZTTOBD 1 | 2 5 | S 0 | 1 | Man Child | | | - | <u> </u> |
| Andykinin Receptor B1 | - 1 | AE103e6 | - | 25 | ¥¥ | CTCCTCTGCCGTGTCATCATCATCATCAAGGCCAATTT | 643 | E | 1,16231.1 | 1690 | 0 | | Slen | | AAC , | AAT NAM 000710.1 | 348 |
| Stechtorin Receptor 61 | - 1 | AE1029.7 | 1 | = | • | GGAAGGCAGCAGCGGCGCAGGAKAGGCCCGGGGTCACCTGCGT | 75 | | 1182311 | 1713 | V 0 | Paris 1 | 170 | | L | Г | |
| handschole Darmoter B+ | - | Attorney | • | | | | | | | | | | 2000 | - | V 000 | AGA NW 000/10.1 | |

| | 1 | | ľ | 1 | | | | | | | | 1 | 118 | , | 040 | A 440 | PAR 000740 1 | ž |
|--------------------------------------|-----------------|-----------|--------------------|------------|----------------------|--|-------------------------|-------------|--------------|---------|--------|-----------|--------------|-------------|-----------|---|------------------------------------|---------|
| Gradenth Heapton 81 | SUKNEY SUCES | AETOSES | BET TO THE CHAPTER | ST CALLED | Transco was to commo | BCC LCC GCCMACGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG | Com a com and a company | OCCUPANT OF | 200 | 900 000 | 1.8 | 1 | į | BENCOMP REF | Ī | CODOMICONA | ALT CODOM COMA SEO NO COMA SEO POS | SEO POS |
| Brachkirin Receptor B2 | _ | AE104e18 | , | 2 | 1 | CTGGGGATTGCAAAATACACGTTCATTCTCCAGCAGGGAGGAG | 199 | - | ALS65102.2 | 68174 | • | D L | | _ | | | | |
| Brachtain Receptor B2 | П | AE104e19 | , | 336 | - | | 25 | 089 | AL255102.2 | 25089 | 0 | Exorg | Менетне | | ZQI | TOT NOW OR | NM 000623.1 | 8 |
| Brachkirian Receptor B2 | BOKHBZ | AE104#20 | | E S | WA | <u> АВОСТТАААОССТТЕСТТЕЛАТВААВАВААСАВАТАВАВТВ</u> | 88 | 5 | ALSS5102.2 | 101078 | ۷ | STRank | Non-CD8 | - | | | - | 1 |
| Brackferin Receptor B2 | BDKRB2 | AE104621 | - | 8 | - | <u> Австетсстеттоставатимуюваететтясястоссте</u> | 88 | 8 | AL365102.2 | 100859 | 8 V | S. Bart | Non-CD3 | + | 1 | + | 1 | T |
| Brachturin Receptor B2 | BOKREZ | A£104e22 | | â | | AGTECTGGGATTTCTTTGTATACGGCACGTACGGCTCCCAAGG | 18 | 126 | ALESSIG22 | 1000 | ٥ ۲ | SR | Non-CCS | + | 1 | + | + | |
| Brachtarin Receptor B2 | ┰ | AE104673 | | 8 | 1 | CATCITICAAGGGATGGGTARVAITGATGTCATCAGCCTCCTGG | 25 | ā | AL\$55102.2 | 100381 | 9 | 4 | Nam COS | - | + | Т | | Ţ |
| Brachetrin Receptor B2 | Т | AE104624 | 1 | £ : | | GAGGGGATCTBTBTGATTACAAGIICGATGGGGCTCBTCCTB | 2 | £ 1 | A.555102.2 | 2882 | 4 | 2 | | ` - | 5 | 200 | M 000003.1 | 8 |
| Brackstein December 82 | BOXOBS | ACIONOS | 1. | 9 5 | - - | TOCACCA A SOCIO CALCACIO CONTROLO CONTR | ě | 8 1 | A1 964102 2 | 1003 | - e | | Managa |] - | ł | Т | M 000623.1 | 95 |
| Proceeding Supergraph Ro | Т | 4510407 | | 1 | - | GOTOOTTOCACTOCACTOCACTTO | 2 | 3 | A1 956102.2 | 62678 | - | L | 800 mg/ | - | - | ¥. | WA 000623.1 | 1877 |
| Brachdarin Receder B2 | Г | AE104628 | | 38 | - | TOCCAGITACGTCTGCGTAATTARATGCCTCACATGTACGTAG | 198 | 8 | ALESSICE 2 | 627.00 | ŀ | Ц | Mon-CD8 | - | H | NA. CA | Ц | 2112 |
| Brachstein Recordor R2 | П | A£104e20 | | 822 | | тамсладтавамаваласамадтамасластататасса | 3 | 8 | ALSSS102.2 | 1,0929 | 4 | Н | Non-CD8 | - | 1 | NAM CK | MA. 000623.1 | 752 |
| Angiolemen Conventing Engyme 2 | AGEZ | A£109e1 | , | \$8 | 0 | ACTIATAGITTTGAAAAAAJCAACACATGGCCTCTCTTCTTC | 3 | Ē | ACCOMPAN 1 | 22189 | ٥ | Introm 4 | Non-COB | - | | 1 | - | |
| Angolemin Converting Excyme 2 | | AE10962 | 9 | 37 | - | TOCABATBTACATATTTACTATCTATBATCTATBBTTTCT | 8 | 25 | ACDCD669.1 | 897796 | ٥ | Intront2 | 100 mg | + | 1 | + | 1 | |
| Angiotensin Converting Entyme 2 | П | A£109cd | ê | 82 | - | GACAAGGAATGGGTGTGAAACGGTTGTCAACTGGGTGTACTCA | 8 | 8 | ACDICAGED.1 | 27989 | o | Parent 3 | Non-CDS | - | 1 | 1 | | |
| Angiotensin Converting Enzyme 2 | ACE | A£100a4 | = | 26 | ۰ | CACTACTAAAAATTAGTAGGCTITACCTGGTTCAAGTAATAAG | 286 | ş | AC003669.1 | 90164 | 0 | Proper | Non-CD8 | - | 1 | | | |
| Anglotensin Conventing Engyms 2 | | AE100e5 | - | ş | 0 | TTTBCTBANGAGAATBCTANTICATAAAGATATCCTTTTGACC | 8 | 586 | ACD000000,1 | 80322 | ٥ | Interes | Nancas | - | | 1 | + | |
| Anglotensin Conventing Enzyme 2 | Z V | AE109e6 | ş | 8 | 0 | GIMATGACTCAGATATGICTITTGGCACACAGAAGACAC | 28 | 965 | ACCOCCEGO,1 | 8113 | 9 | Intront6 | Nam-CD3 | - | - | - | 1 | |
| Anglotensin Converting Enzyme 2 | 2304 | A£100e7 | ş | ž | • | CTAGGAATGATATCAGACACJAGITTTTAGGTGCAGTGACAAA | \$8 | 100 | ACD03689.1 | 84245 | 8 | Exemte | Shra | - | T. | AAC AF241254.1 | + | 2173 |
| Protecte tradition 4 | ¥. | A£110e1 | 7 | 447 | ۰ | ставстствтваествсаадпавтоствтассттстттсат | 8 | 2 | 1.09101.1 | 5990 | - | Internet | Non-CD8 | ۰ | | | | |
| Protesse britisis 4 | ž | A£110e2 | - | 2 | , | AGGACCACTCCCAAAGACTTCTTTATGTTGATGAGAACACAAC | 18 | 88 | 138101.3 | Ę | 0 | Exong | II. | ۰ | Ę | E E | NAL 006215.1 | 8 |
| Protector tradition 4 | 7. | A£110ed | • | ş | | ОСТІВІТСАТТАЛЕТАЛЯПИСТЕЛАСТЕЛАТВОСОСТІТЕ | 88 | æ | 138101.1 | 782 | 1 | Burne | Non-CO8 | ۰ | - | + | + | |
| Protesse tritibitor 4 | ž | AELIDA | - | 8 | | амаетватсталассаластиявттетоввалскалестся | 8 | Ŕ | 1300.1 | 77.00 | - | Introd | Nancos | • | 1 | ┪ | + | |
| Protesse britishs 4 | ž | AE110es | • | \$ | - | AABATTBTBGATTTBGTCAGTTCJAAGACGAAGACGTCTT | £ | Œ | 1300.1 | 3777 | ٥ ۲ | Emmi | Samt | • | TEN | AGC NW C | NAM 006215.1 | 189 |
| Prosesse intellibre | ž | AE110e0 | • | 2 | | CTAAAATAAACTCTGAGGATJA/TGCCATGCTGCATGCAAAATC | · · | ğ | 1,20101.1 | 22.2 | - | a Base | Non-CDB | • | 1 | + | + | |
| Protesses intribitor 4 | ž | AE110e7 | • | ğ | | CATATAAAACACTCCACAAATRIJISTTIBIBAACAAACOCTAA | 8 | ē | 138101.1 | 2002 | 7 | STent | 800-mg | • | | | + | T |
| Protesse inhibitor 4 | ž | AE110m | • | 95 | - | COSQUACCANTICTATOCCCLANGCANCTTTGGGCAGGTCACTT | E | 902 | 1.101.5 | 2844 | 4 | S. Park | 20 | ۰ | 1 | + | $\frac{1}{1}$ | |
| Protection in fablics 4 | ž | AE11000 | - | 88 | 1 | CAACAAACAAACAACAGAAACAAACAAAAAAAAACCA | 924 | 200 | 1300.1 | 922 | 9 | THE S | Man-CD28 | - | + | + | + | 1 |
| Aminopeoliticas P (membrany-bound) | Т | AE1004 | - | ¥ | | CTBTBBCTBCAACCAACCTIC/TACCCABCTTCTTTTCCC | QL, | 863 | ALGENERAL | 99844 | 9 | 1 | SCO-US | • | | 1 | + | T |
| Animopsofidase P (membrane-bound) | Т | AEtopics | 2 | 2 | - | AGTCCACGTTGAAGGTCCGAQGAIBCCCCTAAGCCCTGTGGGGGGC | # | 153 | AL023653.1 | 70606 | 0 | 1 | Mon-CD8 | • | 1 | + | + | T |
| Animopoliticae P (membrane-bound) | Т | AE10028 | 2 | ē | | TTTCTAGGGCCCTGTTGGGGGARCATCCTGTTGTGTGTGTGTAGA | 613 | 82 | AL023653.1 | 70620 | • | _ | Mon-COS | • | | | + | |
| Animopeoplose P (membrane-bound) | XPNPEP2 | AE100427 | = | 112 | | Амаесталссттесма аместа мата семма асма атст | 843 | 82 | AL023653.1 | 65621 | 0 | 4 | SO-CD8 | • | + | | + | |
| Antinoprofiduse P (membrane bound) | т | AE100428 | ξ. | ž | 8 | CCCAAGGGTGCCATGGTCCCTGAAGGGAAAGCCCAAACCTATCAC | š | £ | AL023853.1 | 26087 | 9 | 4 | Mon-CD8 | - | | 1,990724.1 | | 3000 |
| Animoperature P (membrane-bound) | Т | AE100429 | - | 8 | 9 | ACCTATCACCACCTGTTGGGGCTATAGCCAGAGCTGTTCCCAC | 818 | ā | 41.02.0853.1 | 84129 | 5 | ┵ | MonCDS | + | + | Т | ž | 2001 |
| Amnopapticase P (manticare bound) | J | AE1000:30 | z | ¥ | | TBOCTCCTCACCBAOATTCCT/CBCTGGAGGGCGTGTGGGTTT | 816 | ¥ | ALO23653.1 | 61848 | - | 4 | Fig | 4 | + | Т | 1 | ž |
| Brachtern Heceptor B1 | Т | AE100910 | | ğ | 0 | BGTCABCAGGACAAGAGTGCGAAGGGCCGAAGGATAGCAAGA | 917 | 8 | 176231.1 | 8 | ۲ 0 | 4 | Masernes | + | 88 | 8 | MM 000710.1 | 22 |
| Stacytum Heceptor B1 | Т | AE103e11 | | 8 | • | GANTIATCCAAGTGGGCCCTJAGTTATATCACAAGGGTCCTTA | 848 | £ | 112 | Š | 8 | 4 | 80 | - | + | + | | T |
| Gradient Heapon B1 | BLANE) | AE103812 | 1. | | | CHRISTICIAMACICAMAGRACIACIMACICAMACICAMACICAMACICAMACICAMACICAMAGRACIA | 2 1 | 3 | 11. | 200 | - (| + | 200 | - | \dagger | - | + | |
| Prachetin Secretor B1 | 10000 | AS1me14 | - | ž ž | | TOGGTATIONCHICATIONTAL | * 5 | 5 | | 2 | 9 - | 3 | 200 | | ╁ | | | |
| Stachfarin Recessor B2 | Г | AFIOACO | Ĺ | 5 | - | ATACCHITACHIGCHTTAARTHCHCAACACCACTTCATGT | S | 3 | At 9681770 2 | PUICH | , - | L | 800 | - | | 3 | MM 000623.1 | 502 |
| Bradykirán Receptor B2 | П | AETONIST | - | 8 | 0 | Aggoogtgatagacacaaagtygoottcacaaacaaacaaaac | 8 | 3 | A.365102.2 | 00089 | - | ļ. | The state of | - | 86 | OCC NACA | MM_000623.1 | |
| Brachterin Receptor B2 | BOKHBZ | AE104KGZ | 3 | \$ | 0 | TAATAACTBCAAACTBACCTBAAAGTACAGTBAAAAATCAAGC | 100 | 950 | A.365102.2 | 68239 | 8 | L | Mon-CDS | - | Н | | | |
| Brachtfrin Receptor B2 | 80KHB2 | AE 10ects | - | ş | 0 | ATAACTOCAAACTOACCTOAGAATTACAGTOAAAATCAAOCAA | 55 | 198 | AL355102.2 | 68341 | 8 | Introduct | Non-CD8 | - | | | | |
| Brachtinin Receptor B2 | BDKHBZ | AETOMOM | • | 2 | • | CCAATACTGATTCTGCTCCACCTGGAAGTATTTCTAGACCTCA | 88 | ž | A.355102.2 | 52872 | ٥ | Exord | Non-CD8 | - | + | 3 | NA 000623.1 | 2183 |
| Brachtsin Receptor B2 | BDICHBQ | AE10465 | • | ž | • | TECACGGAGCTATTTCTAGNIC/ACTCAGTGTCTTTTCCTTATA | 736 | 596 | AL355102.2 | (2008) | ٥ ٧ | E Sout | Non-CDS | - | 1 | ě | NA 000623,1 | 2167 |
| Brachtanin Receptor B2 | BOICHE | AEtowase | - | 88 | 0 | acacccractosaccarcracatica acaccerrente regional | 123 | 2 | AL\$55102.2 | 62943 | • | 4 | Mon-CDS | - | + | Т | MM 000623.1 | 1012 |
| Professe tradition 4 | ž | AE110e10 | 2 | íŘ | | Accadescrecaecagospacatroscartott | 8 | 598 | 1,38101.1 | 8160 | 0 | 4 | Į. | + | + | Т | NAM 006215.1 | 1149 |
| Protesse Intributor 4 | ž | A£110e11 | + | Ř | | DEGROCCATEGGCTGGAAACA/CATGCGTGGGCAGTGCTCTGTTC | 8 | 35 | 1,28101.1 | 3612 | 3 | 4 | Messres | + | 8 | 20 20 20 20 20 20 20 20 20 20 20 20 20 2 | NAK 006215.1 | 412 |
| Proteste Intibitor 4 | Π | AE110e12 | 1 | <u>\$</u> | | ВАСАВАТВТЕСАТТАТВАВАЕСТВВВТАССАЯТЕТАТССССА | 2 | 298 | 128101.1 | P. | 6 | 1 | 100 mg | - | \dagger | 1 | | |
| Tachykrin Receptor 1 | Τ | AE100e | | 8 | 8 | твассастатататаалтаматеттатаассествалама | 25 | 52 | A0007/400.3 | 141073 | • | 4 | 800 Man COS | + | + | + | $\frac{1}{1}$ | |
| Tachyldrin Necester 1 | J | AE10646 | - | 8 | | BOATATTTETECTAGCTECTCAGCTCTCACAATETEC | 838 | 3 | AC007400.3 | 143385 | ٠ د | 1 | Man CD8 | + | \dagger | + | | T |
| Angidensin Consulting Engine 2 | VOE2 | AE10846 | 8 | 8 8 | - • | AVAILABLE OF THE TOTAL OF THE T | 2 8 | 8 8 | ACCOURAGE ! | SP-03 | | Cluodi 3 | 100 mg | + | \dagger | ╁ | + | Γ |
| Kellouin 1 (renef)perconce/halfvary) | П | AETOTAG | - | 8 | × 0 | GACGCAGGAGTCCCCATC ICT CGCCTTGGGGCTACACAGTCTG | 1574 | 1578 | AFZT7050.1 | 4627 | ╀ | L | Mar CD8 | - ≨ | \vdash | H | | |
| | l | | | | | | | | | | | ı | | | | | | |

| GENE DESCRIPTION | HGNC ID | OI das | HGNC ID SNP ID CONTIG NUM CONTI | 90s | REF. AA ALT AA | LT AN | EXON | MUTATION TYPE REVCOMP | EVCOMP | REF_CODON | ALT_CODON | PROTEIN ID | PROTEIN POS | PROTEIN (SEQ ID NO:) | FLANK_SEO REF (SEQ ID NO:) | FLANK_SEG ALT (SEG ID NO:) | REFSEQ, FLANK REF (SEQ ID NO:) |
|---|---------|-----------------|---------------------------------|------|----------------|-------|--------|-----------------------|--------|-----------|-------------|-------------|-------------|--------------------------|--------------------------------|--------------------------------|------------------------------------|
| Aminopercidase P (membrane-bound) XPNPEP2 AE100s1 | XPNPEP2 | AE100s1 | _ | 8 | ۵ | ٩ | Exon20 | Sllent | ۰ | 8 | 8 | AAB96394.1 | 607 | 7 | 37 | 100 | 163 |
| Bradytinin Receptor B1 | BOKRB1 | BDKRB1 AE103s1 | 89 | 307 | Œ | 0 | Exon2 | Missense | | 080 | CAG | NP_000701.1 | 317 | 8 | 89 | 123 | 186 |
| Bradydnin Receptor B1 | BOKRB1 | BDKRB1 AE103s2 | • | 273 | ۵. | ۵ | Exon2 | Silent | 0 | 800 | V 30 | NP_000701.1 | 41 | 10 | 19 | 124 | 187 |
| Tachykinin Receptor 1 | TACRI | AE106s1 | - | 418 | u. | u | Exon1 | Silent | - | E | υ E | NP_001049.1 | 111 | 16 | 19 | 141 | 207 |
| Tachvidnin Receptor 1 | TACRI | | 2 | 789 | - | _ | Exong | Silent | - | ν | ĄŢĄ | NP_001048.1 | 15 | 81 | 28 | 145 | 208 |
| Techyldrin Receptor 1 | TACRI | AE106s7 | w | 119 | <i>"</i> | ø | Exons | Silent | - | 2 | ž | NP_001049.1 | 378 | R | | 150 | 213 |
| C1 Esterase Inhibitor | P. T. | AE10583 | s | 368 | ø | s | Exon7 | Silent | 0 | AGC | AGT | NP_000053.1 | 406 | 24 | 06 | 153 | 216 |
| C1 Esterase inhibitor | 된 포 | AE10584 | , | 288 | > | < | Exon3 | Missense | 0 | OTT | OCT | NP_000053.1 | 99 | 28 | 94 | 154 | 217 |
| C1 Esterase inhibitor | P. | AE10565 | 7 | 897 | < | o | Exon3 | Missense | | 9CA | - GGA | NP_000053.1 | 159 | 28 | 28 | 155 | 218 |
| C1 Esterase inhibitor | CINH | AE105s8 | 8 | 276 | > | | Exon8 | Missense | 0 | ата | ATG | NP_000053.1 | 480 | 8 | 83 | 156 | 219 |
| Kalikrein 1 (renal/pancreas/salivary) KLK1 | KLK1 | AE10781 | - | 153 | × | E | Exoné | Missense | 0 | AAA | GAA | NP_002248.1 | 186 | 8 | 26 | 157 | 220 |
| Kallikrein 1 (renal/pancreas/salivary) | KLK1 | AE10783 | 2 | 909 | ш | o | Exon3 | Missense | ۰ | GAG | 940 | NP 002248.1 | 145 | 8 | 8 | 159 | 222 |
| Bradytinh Receptor B1 | BOKAB | AE103s8 | - | 67 | z | z | Exon3 | Silent | • | WC | TA | NP_000701.1 | 114 | 925 | 828 | 119 | 643 |
| Bradyldnin Receptor B1 | BOKRB1 | AE103s7 | - | 181 | œ | æ | Exon3 | Silent | ۰ | AGG | AGA. | NP 000701.1 | 152 | 53 | 289 | 612 | 779 |
| Bradykinin Receptor B1 | BOKRB1 | BOKRB1 AE103s8 | - | 296 | _ | ٧ | Exon3 | Missense | ٥ | ств | GTG | NP_000701.1 | 191 | 280 | 581 | 613 | 945 |
| Bradyldnin Receptor B1 | BDKRB1 | BOKRB1 AE103s9 | 2 | 138 | ш | E | Exon3 | Stlent | 0 | GAG | GAA | NP_000701.1 | 233 | 295 | 285 | 614 | 646 |
| Bradyturin Receptor B2 | BOKHB2 | BOKRB2 AE104e19 | 7 | 339 | æ | C | Exori2 | Missense | - | сат | TGT | NP_000614.1 | 14 | 984 | 584 | 616 | 848 |
| Bradyldnin Receptor B2 | BOKRB2 | BDKRB2 AE104824 | * | 918 | 0 | 0 | Exon3 | Silent | - | GAT | GAC | NP_000614.5 | 311 | 995 | 589 | 129 | 653 |
| Bradykinin Receptor B2 | BOKRBZ | BDKRB2 AE104625 | 4 | 1046 | 9 | E | Exon3 | Missense | - | 999 | GAG | NP_000614.1 | 354 | 999 | 280 | 622 | 759 |
| Argiotensin Converting Enzyme 2 | ACE2 | AE109s7 | 15 | 241 | z | z | Exon16 | Silent | - | TA1 | AAC | AAF78220.1 | 989 | 843 | 169 | 833 | 999 |
| Protease Inhibitor 4 | 7 | AE11082 | 2 | 528 | | u. | Exor@ | Slen | 0 | Σ | E | NP 006206.1 | 233 | 2/4 | 88 | 959 | 299 |
| Protease Inhibitor 4 | 7. | AE110s5 | * | 563 | ø | S | Exon1 | Silen | 0 | AGT | AGC | NP_006206.1 | 199 | 9/9 | 909 | 639 | 670 |
| | | | | | | | | | | | 1 | | | | | | |

| | <210><211><211><212><213> | 1576 34 DNA Homo sapiens | |
|--|--|--|----|
| | <400> gcagca | 1576 Igegg eegeetgeae agagtgetge egae | 34 |
| | <400> | DNA Homo sapiens | 34 |
| to the state of th | ~100× | 39 DNA Homo sapiens | 39 |
| | <210><211><211><211><212><213><400>< gcago | > 37 > DNA > Homo sapiens | 37 |

Table VIIA

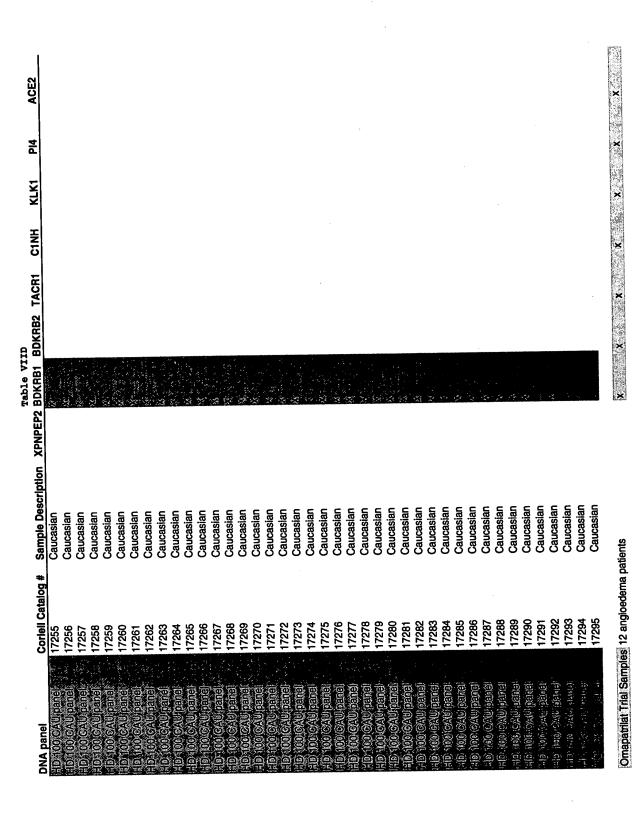
| anel NA14905 anel NA14922 anel NA14923 anel NA14923 anel NA14924 anel NA14925 anel NA14932 anel NA14932 anel NA17202 anel NA17203 anel NA17203 anel NA17205 anel NA17205 anel NA17206 anel NA17206 anel NA17206 anel NA17206 anel NA17206 anel NA17206 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA14686 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1433 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1483 anel NA1433 anel NA1483 anel NA1483 anel NA1483 anel NA14841 anel NA1484 | NA Namel | Corlell Catalog # | Sample Description | XPNPEP2 BDKRB1 | BDKRB2 TACR1 | CINH | KLK1 | P14 | ACE2 |
|--|--|--------------------|--------------------|----------------|---|------------|--------------|-----|------|
| NA14922 AN NA14923 AN NA14923 AN NA14923 AN NA14923 AN NA14923 AN NA14933 AN NA14933 AN NA17203 CC NA17204 CC NA17205 CC NA17205 CC NA17205 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA14683 AN NA14683 AN NA14683 AN NA14683 AN NA14686 AN NA14686 AN NA14696 AN | oriell 24 nanel | NA14905 | African American | × , × | X | × | | | |
| NA14923 A NA14924 A NA14925 A NA14925 A NA14932 A NA14933 A NA14933 A NA17202 C NA17203 C NA17204 C NA17204 C NA17206 C NA17206 C NA17206 C NA17206 C NA17206 C NA17206 C NA17206 C NA17206 C NA17209 C NA14693 D NA14693 D NA14696 A NA14696 | oriell 24 panel | NA14922 | African American | × | × | × | | | |
| NA14924 AA NA14925 AA NA14932 AA NA14933 AA NA14934 AA NA17203 AA17204 CC NA17204 CC NA17205 CC NA17205 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA17206 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14683 CC NA14684 CC NA14684 CC NA14836 CC NA14841 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14836 CC NA14841 CC NA1 | oriell 24 panel | NA14923 | African American | × | × | × | | | |
| NA14925 A NA14932 A NA14933 A NA14934 A NA17203 C NA17204 C NA17205 C NA17206 C NA17206 C NA17206 C NA17206 C NA17206 C NA17207 C NA17207 C NA14683 D NA14683 D NA14684 D NA14683 D NA14684 D NA1468 | oriell 24 panel | NA14924 | African American | × | × | × | | | |
| NA14932 AAA44934 NA14933 AAA4934 AAA44934 AAA44933 AAA44933 AAA44933 AAA44933 AAA4493 AAA444 AA444 | orioli 24 parel | NA14925 | African American | × | × | × | | | |
| NA14933 A NA14934 A NA17202 C NA17203 C NA17204 C NA17205 C NA17206 C NA17206 C NA17206 C NA17207 C NA17208 C NA14683 C NA14683 D NA14683 D NA14684 D NA1468 | oriell 24 nanel | NA14932 | African American | × | × | × | | | |
| NA14334 A NA 17201 C C NA 17202 C C NA 17203 C C C NA 17204 C C C NA 17204 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C NA 17206 C C C C NA 17206 C C C C NA 17206 C C C C C C C C C C C C C C C C C C C | odoli 24 panel | NA14933 | African American | × | × | × | | | |
| NA 17201 NA 17202 NA 17203 NA 17204 C NA 17205 NA 17206 C NA 17209 C NA 17209 C NA 1789 C NA 1483 C NA 1484 C NA 1483 C NA 1483 C NA 1484 C NA 1484 | oriell 24 panel | NA14934 | African American | × | X | × | | | |
| NA17202 NA17203 NA17204 NA17205 NA17206 NA17206 NA17206 ONA17208 ONA17208 ONA17208 ONA17208 ONA17208 ONA17208 ONA17208 ONA17209 ONA14695 ONA14695 ONA14696 O | onell 24 panel | NA 17201 | Caucasian | × | × | × | | | |
| NA17203 NA17204 NA17205 NA17206 NA17206 NA17206 NA17206 NA00576 NA00576 NA00576 NA00576 NA14699 NA14699 NA14699 NA14699 NA14696 NA1 | olieli 24 pariel | NA17202 | Caucasian | × | × | × | | | |
| NA17204 NA17205 NA17205 NA17205 NA17206 NA07206 NA03433 NA07206 NA03433 NA14819 NA14819 NA14819 NA14819 NA14882 NA14883 NA14883 NA14880 NA14880 NA14880 NA14898 NA14880 NA14898 NA14888 | onell 24 panel | NA17203 | Caucasian | × | × | × | | | |
| NA17205 NA17206 NA17208 NA03433 NA06090 NA07426 NA07426 NA07426 NA14819 NA14819 NA14819 NA14682 NA14683 NA14696 NA1469 | Olicii 24 palicii Saioli 24 ponol | NA17204 | Caucasian | X | × | × | | | |
| NA17206 NA17206 NA17206 NA17208 NA00576 NA00576 NA00576 NA14699 NA1 | Ollell 24 pariel | NA1700E | Caucacian | * | × | × | wa.z. | | |
| panel NA17200 Danel NA17200 Danel NA17200 Danel NA07208 Copenel NA07208 Copenel NA07208 Copenel NA07208 Copenel NA07208 Copenel NA07208 Copenel NA07208 Danel NA0720 Danel NA14609 NA14609 Copenel NA14609 Cop | oren za paren | 500Z14N | Couosian | A | × × | × | ***** | | |
| NA17207 NA17208 NA00576 NA00536 NA00536 NA072426 NA072426 NA072426 NA11589 NA11589 NA14683 NA14683 NA14683 NA14688 NA14698 NA1 | orieli 24 panel | NA1/206 | Caucasian | | | * | en er an en | | |
| NA17208 NA00576 NA00576 NA03433 NA04439 NA17208 NA17208 NA14589 NA14683 NA14683 NA14688 NA1 | orieli 24 panel | NA17207 | Caucasian | | | | mmri | | |
| NA00576 C NA03433 NA03433 NA03433 C NA03433 C NA07426 C NA07426 C NA11589 J NA14682 J NA14682 J NA14683 P NA14683 P NA14683 P NA14683 P NA14683 P NA14683 P NA14683 P NA14683 P NA14696 P | oriell 24 panel | NA17208 | Caucasian | * | Y | | (Managerity) | | |
| NA03433 CO NA06090 NA06090 CO NA07426 CO NA07426 CO NA11589 J NA14819 J NA14819 J NA14882 P NA14683 P NA14683 P NA14686 P NA14683 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14696 P NA14699 P NA1469 | orieli 24 panel | NA00576 | Chinese | * | × | * | · · | | |
| NA06090 CON NA07426 NA07426 NA07426 OO NA07426 OO NA11589 JUNA14819 JUNA14682 NA14682 NA14688 NA14686 NA14698 | oriell 24 panel | NA03433 | Chinese | × | * * * * * * * * * * * * * * * * * * * | × | P. Nobella | | |
| NA07426 NA02345b NA11589 NA14819 NA14819 NA14682 NA14682 NA14682 NA14682 NA14682 NA14682 NA14682 NA14682 NA14682 NA14682 NA14683 NA14696 NA14696 NA14704 NA14704 NA14704 NA14704 NA14704 10251 10251 12831 12831 14439 14441 | oriell 24 panel | NA06090 | Chinese | × | × | × | | | |
| NA02345b NA11589 NA14819 NA14672 NA14682 NA14682 NA14696 NA14700 NA14700 NA14700 NA14700 NA14700 NA14700 NA14700 NA14700 NA14700 10251 10378 10378 11439 14441 | oriell 24 nanel | NA07426 | Chinese | × | ××××××××××××××××××××××××××××××××××××××× | × | | | |
| NA11589 J NA11589 J NA14672 J NA14672 J NA14683 J NA14696 J NA14700 J NA14700 J NA14700 J NA14700 J NA14700 J NA14700 J NA14700 J NA14700 J NA14700 J NA1470 | olicii Et pariol | NACCORE | lananaca | × × | × | × | | | |
| NA11589 NA14819 NA14682 NA14683 NA14696 NA14696 NA14696 NA14696 NA14696 NA14696 NA14696 NA14696 NA14699 NA1469 NA1469 NA1469 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 NA1489 | oneli 24 panel | OCHCONN OCHCONN | Japanoso | 4 | X | * | | | |
| NA14819 NA04535 NA14682 NA14683 NA14686 NA14696 NA14696 NA14696 NA14700 NA14700 NA1460 S865 T754 10251 10378 14439 14441 | oriell 24 panel | NA11589 | Japanese | < | | • | | | |
| NA04535 J NA14672 P NA14683 P NA14683 P NA14696 NA14696 NA14696 P NA14696 P NA14700 NA14696 P NA14700 P NA14700 P NA1469 | oriell 24 panel | NA14819 | Japanese | × | < : | ć 3 | | | |
| NA14672 NA14683 NA14683 NA14688 NA14698 NA14698 NA14698 NA14704 NA14704 NA14704 NA14704 NA14704 NA1470 NA14 | oriell 24 panel | NA04535 | Japanese | × | * | | | | |
| NA14682 NA14683 NA14696 NA14698 NA14698 NA14704 NA1470 | (4,431) (3,152374) | NA14672 | African American | | | | | | |
| NA14683 | Halling School | NA14682 | African American | | | | | | |
| NA14696 Petrol NA14698 NA14698 NA14698 NA14700 NA14704 NA14706 NA1470 | (भारति हैं। अस्ति। | NA14683 | African American | | | | | | |
| NA14698 NA14700 NA14700 NA14700 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14704 NA14706 NA1470 | Mercall & Mean | NA14696 | African American | | • | | | | |
| NA14700 NA14704 NA147 | Contract to Mental | NA14698 | African American | | | | | | |
| NA14704 NA14704 NA1850 Spanel 3382 Spanel 3725 Spanel 10251 Nganel 10378 Spanel 12931 Spanel 12931 Spanel 1439 Spanel 14439 Spanel 14439 | Charles & Highly | NA14700 | African American | | | | | | |
| NA1850 | 39-34 \$ 1.01-131 | NA14704 | African American | | | | | | |
| () () () () () () () () () () () () () (| In the Assessing | NA1850 | African American | | | | | | |
| 125 | | 3382 | African American | 212 | | | | | |
| (A) period (B65 (A) period (B65 (A) period (B65 (A) period (B65 (B65 (B65 (B65 (B65 (B65 (B65 (B65 | JENERAL MAN GRADAM | 3725 | African American | | | | | | |
| (%) [gaine] 7754 (%) [gaine] 10251 (%) [gaine] 10378 (%) [gaine] 12931 (%) [gaine] 13294 (%) [gaine] 14439 (%) [gaine] 14441 (%) [gaine] 14441 | | 6965 6965 | African American | ž | | | | | |
| AND panel (754 AND panel (754 AND panel (755 AND pa | Ş | 9993 | African American | | | | | | |
| 50 AA panel 10251 50 AA panel 10378 50 AA panel 12931 50 AA panel 13294 50 AA panel 14439 51 AA panel 14441 51 AA panel 14441 | 3 | 7754 | Amcan American | | - | | | | |
| 10378 12931 13294 14439 14441 14454 | (500 A)A) | 10251 | African American | ×× | | | | | |
| 12931 13294 14439 14441 14454 | | 10378 | African American | €2. | | | | | |
| 13294 14439 14441 14454 | 5 (b) (5(b) /3/3/ [BEINTE] | 12931 | African American | × | | | | | |
| 14439 14441 14454 | A Sold Control of the | 13294 | African American | · | | | | | |
| 14441 14454 14464 | #(D) (\$(0, \dagger) (6) (6) (1) | 14439 | African American | | | | | | |
| 14454 | TO SO AS INSTE | 14441 | African American | | | | | | |
| 14464 | A STATE OF S | 14454 | African American | : / | | | | | |
| | The Street Street Street | 14464 | African American | * | | | | | |

Table VIIB

| DNA panel | Coriell Catalog # | Sample Description | XPNPEP2 BDKRB1 | BDKRB2 TA | TACR1 | SINH | KLK1 | PI4 | ACE2 |
|--|-------------------|--------------------|-----------------------------|-----------|-------|------|------|-----|------|
| Sarrelphy (1) | 14537 | African American | Section Section 2 to 1 to 1 | | | | | | |
| d | 14583 | African American | | | | | | | |
| 4 Annamel No. 1888 | 14681 | African American | | | | | | | |
| HD 50/44 panel | 14687 | African American | | | | | | | |
| * | 14697 | African American | | | | | | | |
| (alue) | 14699 | African American | | | | | | | |
| Ampainel M. | 14720 | African American | | | | | | | |
| W. panel | 14746 | African American | | | | | | | |
| W. feathell | 14754 | African American | | | | | | | |
| AN partel | 14755 | African American | | | | | | | |
| Manage) | 14771 | African American | | | | | | | |
| Plo/So/Axx panel | 14772 | African American | | | | | | | |
| With the same of t | 14783 | African American | | | | | | | |
| | 14826 | African American | | | | | | | |
| HID SOVAN PERIOR | 14837 | African American | | | | | | | |
| HIDEO/AVAIDAME! | 14862 | African American | | | | | | | |
| | 14863 | African American | | | | | | | |
| Walestell | 14864 | African American | | | | | | | |
| (4,(b),500,440, permel! | 14892 | African American | 200 | | | | | | |
| (A) Netucil | 14893 | African American | 2 2 3 | | | | | | |
| | 14894 | African American | <i>`\$8</i> | | | | | | |
| | 14895 | African American | 2.4 | | | | | | |
| HID GO WYN DEIDEI | 14897 | African American | | | | | | | |
| HDGO/ANganel | 14900 | African American | | | | | | | |
| (400,500,4%) peintel | 14901 | African American | : | | | | | | |
| HDGOAN peinel | 14903 | African American | | | | | | | |
| HD GO AVIDERADI | 14904 | African American | | | | | | | |
| HD 500公公良官和司 | 14905 | African American | | • | | | | | |
| 10) 00 47% period | 14922 | African American | · · · | | | | | | |
| HDEO (W) DEUTS | 14923 | African American | × | | | | | | |
| 14(0)/4(0)/4/4/(05)(0) | 14924 | African American | | | | | | | |
| HID SOLVA paintel | 14925 | African American | 14 | | | | | | |
| KDECKY, ISSNE! | 14932 | African American | 34 | | | | | | |
| HIDVED AND GENERAL | 14933 | African American | 1. | | | | | | |
| HD HEED GROUP SERVER | NA 17201 | Caucasian | | | | | | | |
| TENERAL MARKET THE | 17202 | Caucasian | *** | | | | | | |
| | 17203 | Caucasian | | | | | | | |
| HILL HOT HEAD CHANGED HELD | 17204 | Caucasian | * | | | | | | |
| HE NOW GANGERE | 17205 | Caucasian | 150 | | | | | | |
| INTERNATION OF STREET | 17206 | Caucasian |) (2) (2) | | | | | | |
| AND TOTAL CONTRIBUTION | 17207 | Caucasian | ** | | | | | | |
| Migrafill March Spar of the | 17208 | Caucasian | | | | | | | |
| न्तिमानेविक्ति क्रिक्ति क्रिक्ति | 17209 | Caucasian | <i>-</i> | | | | | | |
| the court of | 17210 | Caucasian | | | | | | | |

Table VIIC

| | Towner to the state of the stat | O-maning. | 2000 | | | |
|--|--|-----------|--|---|--|--|
| HIDE OF CAUSTINES | 17211 | Caucasian | | | | |
| | 17212 | Caucasian | | | | |
| (#IB/FIGOROAU) FERREIN | 17213 | Caucasian | | | | |
| | 17214 | Caucasian | | | | |
| S B (((C) (C) () (orange) | 17215 | Caucasian | | | | |
| Hinanio Callingane | 17216 | Caucasian | | | | |
| HIB (1010) CANUTOENED | 17217 | Caucasian | | | | |
| Halby (of Cyturosine) | 17218 | Caucasian | 100 M | | | |
| (In) (010 (CAND) apprel | 17219 | Caucasian | 100000000000000000000000000000000000000 | | | |
| | 17220 | Caucasian | | | | |
| 112) 1000 (e) (VIVe (21)(2) | 17221 | Caucasian | 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1 | | | |
| (Fig. 100) CAU internel | 17222 | Caucasian | 120 | | | |
| | 17223 | Caucasian | 25. | | | |
| "in him (extilinative) | 17224 | Caucasian | | | | |
| | 17225 | Caucasian | | | | |
| | 17226 | Caucasian | | | | |
| | 17227 | Caucasian | | | | |
| ATD-1800 GANUS ESTEDI | 17228 | Caucasian | | | | |
| + | 17229 | Caucasian | *** | | | |
| | 17230 | Caucasian | | | | |
| | 17231 | Caucasian | | | | |
| | 17232 | Caucasian | The state of the s | | | |
| (alb) victor & NU period | 17233 | Caucasian | · · · · · · · · · · · · · · · · · · · | | | |
| HE THOUGHAND PETATEL | 17234 | Caucasian | × | | | |
| | 17235 | Caucasian | * | | | |
| HED VIEW CARD (DETACT) | 17236 | Caucasian | Xe. | | | |
| | 17237 | Caucasian | | | | |
| 1-10/100/04/04/05/1001 | 17238 | Caucasian | × . | | | |
| | 17239 | Caucasian | *** | | | |
| HEWATHER MANAGEMENT | | Caucasian | | | | |
| | | Caucasian | 763 | | | |
| In TO THE CONTRIBUTION | | Caucasian | : | | | |
| IND NOTE CONTRIBUTED. | | Caucasian | | | | |
| (Enternational County) | 17244 | Caucasian | XX. | | | |
| PARTIE CANUFERRIE | 17245 | Caucasian | | | | |
| HE WINGSTON | 17246 | Caucasian | ×× | | | |
| (E)VECTION (A) (A) (A) (A) (A) (A) (A) (A) (A) (A) | 17247 | Caucasian | ** | | | |
| HE HOLD TOUR CONTROLLEGATION | 17248 | Caucasian | × | | | |
| A 19 THOUSE CONTROL PERMENT | 17249 | Caucasian | | | | |
| HE HOUSE CANNIFORMS | 17250 | Caucasian | ** | | | |
| (4) (0) (0) (0) (0) (0) (0) (0) | 17251 | Caucasian | | ٠ | | |
| Handillan needs (class | 17252 | Caucasian | 24 | | | |
| Lafter water Constitution of Lat | 17253 | Caucasian | 2 | | | |
| Contact Contact State Contact | 17254 | Caucasian | | | | |



| GENE DESCRIPTION | HGNC ID | OI das | EXON | REVCOMP | PCR Amplicon Name | Target Name | PCH Left primer | (SECTIONO:) | PCR Right primer | (0.00) |
|--|---------|----------|---------------|---------|-------------------|-----------------|-------------------------|-------------|------------------------|--------|
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s1 | Exon20 | 0 | AE100p77p78 | XPNPEP2_X20a | AGTGCTCCTTCCTTC | 297 | TATTCACTACCTGGGGTTGGG | 360 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s2 | Intron3 | 0 | AE100p9p10 | XPNPEP2_X3a | CAGCCCAGGCATCTTAATCTA | 298 | TCTCTACTTCCCTCCCTTTGC | 381 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s3 | Intron15 | 0 | AE100p57p58 | XPNPEP2_X15a | TAGCTGTCTTCTTCCTTTCGC | 588 | ATAGGATGAGGCTCAGCTTGG | 382 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s4 | Intron15 | 0 | AE100p57p58 | XPNPEP2_X15a | TAGCTGTCTTCTTCGC | 300 | ATAGGATGAGGCTCAGCTTGG | 383 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s5 | Intron1 | 0 | AE100p1p2 | XPNPEP2_X18 | TGATTGAGACCAGCTGTTGTG | 301 | AACAGAAAAAGAGACTCGGGC | 8 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s6 | Intron7 | 0 | AE100p25p26 | XPNPEP2_X78 | CCAGCGTGGGCATACATG | 305 | GGCCCTGAAATCTGCATTT | 88 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s7 | Intron7 | ٥ | AE100p25p26 | XPNPEP2_X78 | CCAGCGTGGCCATACATG | 303 | GGCCCIGAAICIGCAIII | 88 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s8 | Intron10 | 0 | AE100p37p38 | XPNPEP2 X10a | CTTCCTTTGACCTCCAGGAAC | 8 | CCIGITICCICITICIBECICI | 28.6 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s9 | Intron10 | 0 | AE100p37p38 | XPNPEP2_X108 | CHICCHIGACCICCAGGAAC | 58 | COLGITICALATORICICI | 960 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s10 | Intron7 | 0 | AE100p25p26 | XPNPEP2 X/8 | CCAGCGIGGGCAIACAIG | 350 | CACCITCTCAGGCCTTTTCATT | 370 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100811 | Intron13 | 0 | AE100949950 | XPNPEPZ X138 | TANATONONOTONO | 300 | CAGCICICAGGCCTTTCATT | 371 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s12 | Introntia | ٥ | AE100p49p50 | XPNPEP2 X138 | TANATOROGOTOR | 900 | CAGCTCTCAGGCCTTTTCATT | 37.5 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s13 | Intron13 | ٥ | AE100P49p50 | XPNPEPZ X138 | TOATTO ACACCAGGICAGGICA | 340 | AACAGAAAAAGAGACTCGGGC | 373 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100814 | Exon1 | ٥ | AETOOPTE | XPNPEPZ X18 | TOTTOTO ACCAGCIGITOTO | 310 | AACAGAAAAAAACTCGGGC | 97.6 |
| Aminopepidase P (memorane-bound) | XPNPEPZ | AE100815 | Exon | - | AE100pip2 | VENDEDO VOS | GOOCCATGTCATTAATGAGTAC | 343 | TCAGGGCTACCTTTGTCCTT | 375 |
| Aminopepudase P (membrane-bound) | VENDEDS | AE100S10 | 1moons | | AETODESPSO | YDNDED2 X17a | COCTOTTOTTAGGCACCACTC | 343 | CTGCTGGCATTCCTCACTTAC | 376 |
| Aminopolitiese P (membrane-bound) | XPNPEPS | AF100s17 | Intron17 | | AE100ps3000 | XPNPFP2 X17a | CCCTCTTCTTAGGCACCACTC | 314 | CTGCTGGCATTCCTCACTTAC | 377 |
| Aminopentidase P (membrane-bound) | XPNPEPS | AE100s19 | (mton15 | , | AE100057058 | XPNPEP2 X15a | TAGCTGTCTTCTTCGC | 315 | ATAGGATGAGGCTCAGCTTGG | 378 |
| Aminopeptidase P (membrane bound) | XPNPEP2 | AE100s20 | Intron21 | • | AE100p81p82 | XPNPEP2_X21.f18 | GGACTATGGTGACAGCTGGAG | 316 | CAAGAAGCCCTGTGTTCCTG | 379 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s21 | Exon21 | • | AE100p81p82 | XPNPEP2_X21.f18 | GGACTATGGTGACAGCTGGAG | 317 | CAAGAAGCCCTGTGTTCCTG | 380 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s22 | Exon21 | • | AE100p85p86 | XPNPEP2_X21.f28 | GAGGCTCCAGACTCTCCTGTT | 318 | TTAGGAATGATGGGTTCACATG | 381 |
| Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s23 | Exon21 | 0 | AE100p85p86 | XPNPEP2_X21.f2a | GAGGCTCCAGACTCTCCTGTT | 319 | TTAGGAATGATGGGTTCACATG | 385 |
| Bradykinin Receptor B1 | BDKRB1 | AE103s1 | Exon2 | 0 | AE103p13p14 | U48231_X2.13a | CACTTTGCAAGGATTGTGGAG | 320 | AAGAAAGCCAAGCTTCTTGGT | 383 |
| Bradykinin Receptor B1 | BDKRB1 | AE103s2 | Exort2 | 0 | AE103p5p6 | U48231_X2.f18 | TGGCTCTGTGCCAATAAAACT | 321 | CACCACCAGGAAGATGCTG | 8 |
| Bradykinin Receptor B1 | BOKRB1 | AE103s3 | Exon3 | ٥ | AE103p17p18 | U48231_X2.f4a | AGGACCAAGGTCTGGGAACT | 88 | TGGAGGCCAGAATCCTAAAT | 88 |
| Bradykinin Receptor B1 | BDKRB1 | AE103s4 | Exon1 | ٥ | AE103p1p2 | U48231_X18 | GCTGCCAGGAAGATTAAATGA | 883 | ATCTCAGTACTTTGGGAGGCC | 98 |
| Bradykinin Receptor B1 | BDKRB1 | AE10385 | Exon3 | ۰ | AE103p25p26 | U48231_X2.16a | ACTICCCAGACICAAGGGAIC | 25.0 | CGIGGIGIGICAIGCAAII | 36/ |
| Bradykinm Heceptor B2 | BUKHEK | AE10481 | Luciu | - . | AE10453534 | BUKHBZ ATINB | CGACTAGGICCICACCAGACA | 353 | CTCAGTGTCCAGGGAAATGC | 88 |
| Bradykinin Heceptor BZ | BUKHBK | AE1048Z | Intron 1 | - - | AE104535540 | BUNNEZ ALLIB | COACCAAATACCACACACA | 200 | CCGAGGTTCTCTGGAGAAAA | 360 |
| Brachfrin Boomtor Bo | BUKBBS | AF104e4 | industrial in | - | AE104n39n40 | BUKRR X1 19 | GCAGGCAAATACCACTTTCAA | 800 | CCGAGGTTCTCTGGAGAAAA | 391 |
| Bradykinin Recentor B2 | BDKRB2 | AE10485 | Infront | - | AE104n39n40 | BDKRB2 X1.12 | GCAGGCAAATACCACTTCAA | 329 | CCGAGGTTCTCTGGAGAAAAA | 392 |
| Bradykinin Receptor B2 | BDKRB2 | AE10456 | Intron1 | - | AE104p39p40 | BDKRB2 X1.12 | GCAGGCAAATACCACTTTCAA | 330 | CCGAGGTTCTCTGGAGAAAA | 393 |
| Bradykinin Receptor B2 | BOKRB2 | AE104s7 | Intron2 | - | AE104p29p30 | BDKRB2 X2a | GCTCTTTCTGGAAGGTCCACT | 331 | ATACCAACAGCTTCCCCAGTT | 394 |
| Bradykinin Receptor B2 | BDKRB2 | AE10458 | Exon3 | - | AE104p25p26 | BDKRB2 X3.f7a | GETCTCAGCACTGTGATCCTC | 332 | CAAAGACTCAAGTGGGAACGA | 395 |
| Bradykinin Receptor B2 | BDKRB2 | AE10489 | Exon3 | - | | BDKRB2_X3.f7a | GGTCTCAGCACTGTGATCCTC | 333 | CAAAGACTCAAGTGGGAACGA | 396 |
| Bradyldnin Receptor B2 | BOKRB2 | AE104s10 | Exor3 | 1 | AE104p25p26 | BDKRB2_X3.f7a | GETCTCAGCACTGTGATCCTC | 334 | CAAAGACTCAAGTGGGAACGA | 397 |
| Bradykinin Receptor B2 | BDK RB2 | AE104s11 | Exon3 | - | AE104p9p10 | BDKRB2 X3.f3a | TCTACATGCCAGAAGCCTGTT | 336 | CCACTCTCCTCTGCTCAGTA | 388 |
| Bradydnin Receptor B2 | BOKHB2 | AE104812 | Exoug | - | AE104p9p10 | BDKHB2_X3.f3a | ICIACA IGCCAGAGGCCIGII | 98 | CCACICICCICIGCCICAGIA | 288 |
| Bradydnin Heceptor B2 | BUKHBZ | AE104813 | Exous | - | AE10409D10 | BUKHB2 X3.R8 | ICIACA IGCCAGAAGCCIGII | 25/2 | CCACACATCACTATTGGGAGCC | 401 |
| Dradding Doorsto Do | BOKEBE | AE104814 | S, Clark | - - | AE104p21p22 | BURNEZ ASJOS | ACTTANTECTTEGGTGATGAA | 230 | CTAGAATCATAGGCGCAGCAG | 402 |
| Brachkinin Recentor R2 | BOKRB | AF104e17 | S Flank | - | AF104n3n4 | ROKERS X3.f1 | GCTTAATGCTTGGGTGATGAA | 340 | CTAGAATCATAGGCGCAGCAG | 403 |
| Tachvidnin Receptor 1 | TACR1 | AE106s1 | Exont | - | AE106p23p24 | TACR1 X1.ff | CGTGGTCCTCTATGAGCACTT | 38. | CATCTCCACTAACACCTCGGA | 404 |
| Tachyldinin Receptor 1 | TACR1 | AE106s2 | Exon2 | _ | AE106p17p18 | TACR1_X2a | GGGTATATGTGAGAAATGCTTGC | 342 | TCATCAGGAATCAAAGGGTTTC | 405 |
| Tachydnin Receptor 1 | TACRI | AE106s3 | Intron3 | - | AE106p13p14 | TACR1_X38 | CTGGGTTCCAAAGACACTGAA | 343 | TATGCAGGTGACAAGTCTCCC | 406 |
| Techykinin Receptor 1 | TACRI | AE106s4 | Exon5 | - | AE106p1p2 | TACR1_X5.f1a | CTGCAGGAGGCTAATCTGAGA | 344 | TCCAACTGCTCTTCACGAAGI | /04 |
| Tachykinin Receptor 1 | TACRI | AE106s5 | Exons | - | AE106p1p2 | TACR1 X5.118 | CTGCAGGAGGCTAATCTGAGA | 98 | TOCAACTCCTCTTCACGAAGT | 408 |
| Technician December | TACE | AE10050 | Cross | | AETOPTOS | TACEL ASSIB | ACCCATACTGACCITTTTGC | 247 | TAACAAGCTGATGCAGTGGTG | 410 |
| C1 Estense Inhibitor | HNEO | AF105e1 | Junuary 1 | - - | AF105017018 | CINH X4s | AATACCCTCCATTCCAGCCT | 5 58 | TGGAGTGACCTAATGCTCCTG | 411 |
| C1 Esterase Inhibitor | CINH | AE105s2 | Introne | | AE105p25p26 | CINH X68 | GTCTTCCCATTCTGGGTCCT | 349 | GGTGGAAATACAGATGGAAGGA | 412 |
| C1 Esterase Inhibitor | CINH | AE105s3 | Exon7 | 0 | AE105p29p30 | C1NH_X7a | CACTGTTCACCCAGCTGGTAT | 350 | ACATCTTAGGGATCCCCTTT | 413 |
| l Esterase | CINH | AE10594 | Exon3 | 0 | AE105p9p10 | C1NH_X3.f1a | AGATTGCTCATCTGCTGCACT | 321 | AGTAGTGGGCTGGGTAGGAGA | 414 |
| C1 Esterase Inhibitor | CHNH | AE105s5 | Exon3 | 0 | AE105p13p14 | CINH X3.f2a | TTCAGCCACCAAATAACAGC | 382 | TGGATTGGTGACTCTTATGGG | 415 |
| C1 Esterase inhibitor | CINH | AE10588 | Exon8 | ٥ | AE105p33p34 | CINH X8.na | GAACCCAGAGAIICAGGACA | 3 | GIGGAIAGCGGACACCIGAG | 417 |
| Kanikain ((enal/panceas/saivaiv) | VIV. | AE10/81 | Exon | | AE107013014 | KIKI X48 | GACTACAGCCACGACCTCATG | 36.5 | GCTCTCAGAAGCCAGTTCAGA | 418 |
| Kalikrein 1 (renal/hancreas/selivery) | KIKI | AF10783 | Exon3 | • | AE107013014 | KIK1 X48 | GACTACAGCCACGACCTCATG | 356 | GCTCTCAGAAGCCAGTTCAGA | 419 |
| Kalikrein 1 (renal/bancreas/salivary) | ğ | AE10784 | InfromA | | AE107p13p14 | KLK1 X4a | GACTACAGCCACGACCTCATG | 357 | GCTCTCAGAAGCCAGTTCAGA | 420 |
| Kallikrein 1 (renal/pancreas/salivary) | KUK1 | AE10785 | 3' Flank | 0 | AE107p17p18 | KLK1 X5a | GCTCCCCAGGCAGAACTT | 956 | CTGCTGGTGACCTCAGACTTC | 421 |
| | | | | | | | | | | |

| CONTIGNATION CON | GENE_DESCRIPTION | HGNC_ID | SNP_ID | EXON | TEXCOMP. | PCH Amplicon Name | BURN 1951B | PCR Left primer | (SEQ ID NO:) | PCR Right primer | (SEQ ID N |
|--|-------------------------------------|-----------------|----------|----------------|----------|-------------------|-----------------|--|--------------|--|---|
| March Marc | 3radykinin Receptor B1 | BDKRB1 | AE103s6 | Exon3 | 0 | AE103p9p10 | U48231_X2.f2a | GCCTCTGATCTGGTGTTTGTC | 707 | CTGTGGTCTTGCTATCCTTCG | 12 |
| Secretary Actions Excess Control Con | 3radykinin Receptor B1 | BDKRB1 | AE103s7 | Exon3 | ٥ | AE103p9p10 | U48231 X2.f2a | GCCTCTGATCTGGTGTTTGTC | 708 | CTGTGGTCTTGCTATCCTTCG | ľ |
| BINNERS A CHILDEN PRINTER CONTROLLED | 3radykinin Receptor B1 | BDKRB1 | AE103s8 | Exon3 | ۰ | AE103p9p10 | U48231 X2.12a | GCCTCTGATCTGGTGTTTGTC | 709 | CTGTGGTCTTGCTATCCTTCG | ľ |
| BOTONIES ACCOUNTY CONTRICTORY CONTRI | 3radyldnin Receptor B1 | BDKRB1 | AE103s9 | Exon3 | • | AE103p13p14 | U48231 X2.f3a | CACTTTGCAAGGATTGTGGAG | 710 | AAGAAAGCCAAGCTTCTTGGT | ľ |
| BYONES KENNEN KENNEN STATE KENNEN STATE KENNEN STATE | Stadyldnin Receptor B2 | BDKRB2 | AE104s18 | Intron1 or Exo | - | AE104p65p66 | BDKRB2 X3-5a | GGCAGGCAGGAATTAGTCT | 711 | AGATCCAGACAGAGGAGGG | ľ |
| BONDER KINDER KINDER STATE THE REPORTED BONDER N'Y THE TRANSPORTED BONDER N'Y THE TRANSPO | 3radykirán Receptor B2 | BDKRB2 | AE104819 | Exon2 | - | AE104p65p66 | BDKRB2 X3-5a | GGCAGGCAGGAATTAGTCT | 712 | AGATCCAGACAGAGAGGGG | ľ |
| 100.002 | 3radykinin Receptor B2 | BDKRB2 | AE104s20 | 5'Flank | - | AE104p89p90 | BDKRB2 x1-3a | CTGGGATTTCTTTGTATGCCA | 713 | AGAGCCTACAGCCAGTTCACA | |
| BONES A. F. EMAN S. The Print A. F. EUGOSTON BONES X14 A. CONTOCIO CONTOCIO THE A. CONTOCIO CONTOCIO CONTOCIO CONTOCIO A. CONTOCIO CONT | Pradykinin Receptor B2 | BDKRB2 | AE104s21 | 5'Flank | - | AE104p89p90 | BDKRB2_x1-3a | CTGGGATTTCTTTGTATGCCA | 714 | AGAGCCTACAGCCAGTTCACA | |
| Monest Control Contr | Bradykinin Receptor B2 | BDKRB2 | AE104s22 | 5'Flank | - | AE104p87p88 | BDKRB2_X1-2 | ACCTTCGCTCTCCGCTCT | 715 | AGAAACCTCCGCCATACATCT | ľ |
| BONNER KEINAGA ENGINE MATERIAN MAT | Bradykinin Receptor B2 | BDKRB2 | AE104s23 | 5'Flank | 1 | AE104p81p82 | BDKRB2_X1-18 | ACGACCACAGGGAAACTTCTC | 718 | GAGGACGTITITGCCGTC | _ |
| BONNER K. F. LONGE Early 1 K. F. LONGER S. N. S. G. COCCUPACIONALINATION 71 GASTICOTOCOLOGICAL STATES GASTICOCOLOGICAL STATES GASTICOCOLOG | Fradykinin Receptor B2 | BDKRB2 | AE104s24 | Exon3 | | AE104p65p66 | BDKRB2_X3-5a | GGCAGGGCAGGAATTAGTCT | 717 | AGATCCAGACAGAGGGGGG | Ľ |
| BORNER A. F. F. LONG Early A. F. F. L. F. F. L. L. L. L. L. L. L. L. L. L. L. L. L. | 3radykinin Receptor B2 | BDKRB2 | AE104s25 | Exon3 | 1 | AE104p65p66 | BDKRB2_X3-5a | GGCAGGCAGGAATTAGTCT | 718 | AGATCCAGACAGAGGGGGG | _ |
| December Control Event Control Contr | 3radykinin Receptor B2 | BDKRB2 | AE104s26 | Exon3 | 1 | AE104p61p62 | BDKRB2_x3-4a | GACCTCCTTGTCCATCAGTGA | 719 | GGGCTGCTGTGAATTTGTGTA | 1 |
| Potential Evolutia Evoluti | 3radykinin Receptor B2 | BDKRB2 | AE104s27 | Exon3 | 1 | AE104p57p58 | BDKRB2_X3-3a | TCCCAGTTACGTCTGCGTAAT | 720 | GCTGAGTGCACAAGTGAGTTG | _ |
| MEDICATION ATE NAME OF THE CONTRICTORY MACROAL MACCOAL | Bradykinin Receptor B2 | BDKRB2 | AE104s28 | Exon3 | • | AE104p53p54 | BDKRB2_X3-2a | GCCACCTTCCAATAAACCATT | 721 | GGGTGATATGGACAGCAGAAG | 2 |
| ACREST ACRIDATE ACRIBATION OF ACTIONS THOROCONTICOLOGICAL AND ACTION OF THE ACTION | 3radyldriin Receptor B2 | BDKRB2 | AE104s29 | Exon3 | - | AE104p53p54 | BDKRB2_X3-2a | I GCCACCTTCCAATAAACCATT | 722 | GGGTGATATGGACAGCAGAAG | 7 |
| M.22 ACTORNAL MARCONAL AND ACTORNAL ACTORNAL AND ACTORNAL ACTO | Anglotensin Converting Enzyme 2 | ACE2 | AE109s1 | Intron14 | - | AE109p25p26 | ACE2_x148 | TTAAAAACCCAAAGCCAAAGG | 723 | TTCTCGTTTTCCAAAAGCCT | 2 |
| KA22 ACTORNAM (ACTORNAM CONTROLL) ACTORNAM (ACTORNAM CONTROLL) 725 ACTORNAM (ACTORNAM CONTROLL) ACTORNAM (ACTORNAM CONTROLL) 725 ACTORNAM (ACTORNAM CONTROLL) ACTORNAM (ACTORNAM CONTROLL) 725 ACTORNAM (ACTORNAM CONTROLL) 725 ACTORNAM (ACTORNAM CONTROLL) 725 ACTORNAM (ACTORNAM CONTROLL) 725 | Angiotensin Converting Enzyme 2 | ACE2 | AE109s2 | Intron12 | + | AE109p29p30 | ACE2_x138 | CACCATAGCAGAGAAGAAGCA | 724 | GCCAAGTCAAAGAGAAGAAACC | 7 |
| ACES ACT (1986) TATE (1986) ACT (1986) TATE (1986) ACT (1986) TATE (1986) ACT (1986) TATE | Anglotensin Converting Enzyme 2 | ACE2 | AE10983 | Intron13 | - | AE109p29p30 | ACE2_x13a | CACCATAGCAGAGAAGAAGCA | 725 | GCCAAGTCAAAGAGAAGAACC | , |
| March Marc | Angorensin Converting Enzyme 2 | ACEZ | AE10954 | Intron3 | - | AE109p69p70 | ACE2_x3a | GTAAGGTTGGCAGACATCAGG | 726 | AAAAATCATGTGGTCAAAAGGA | |
| Marie Mari | Angulensin Converting Enzyme 2 | ACE2 | AE10985 | Intron2 | - | AE109p69p70 | ACE2_x3a | GTAAGGTTGGCAGACATCAGG | 727 | AAAAATCATGTGGTCAAAAGGA | |
| Control Cont | Angolenism Contenting Enzyme 2 | ACE2 | AE10956 | mron16 | - | AE109p17p18 | ACE2_x18a | CTGTGGGATCCTTCTGGAATT | 728 | CAATTACATCCTCTCATTGTTTGC | |
| Part | Angeles and College and Cricyline 2 | 27.6 | AE1098/ | Exonio | - - | AE109p17p18 | ACE2_X168 | CIGIGGGAICCHCIGGAAII | 62/ | CAALIACATCCTCTCATTGTTTGC |] |
| Control Cont | Totales Intibitor 4 | 2.0 | AE11081 | Luon1 | 0 | AE110p21p22 | Pl4 X2a | GGACATCTTGATGGGCTCATA | 730 | TGGGGCACTGTCTTTCATTAG | |
| Hearth | Protesse Inhibitor 4 | ž d | AE11082 | Patrons | | AE110p21p22 | F14_X28 | GGACAICHGAIGGGCICAIA | 15/2 | IGGGCCACIGICITICATIAG | |
| Header H | Protesses Inhibitor 4 | 70 | AE11055 | The Control | | AE I TOPZOPZO | LIA VIII | GCCIGGGIACAAGGAACCI | 735 | CCGAGIICICIAGGGAIIGCI | ľ |
| PH | Protesse Inhibitor 4 | 710 | AETTOR | Event | | AE110p25p26 | F14 A38 | GCCIGGGIACAAAGGAACCI | 3 | CCGAGI ICI CI AGGGAI I GCI | |
| PH | Professe inhibitor 4 | 7id | AF110eR | S'Elank | | AE110NENG | DC 14 10 | TAGAAGGTTTTGGGGTGAGA | 100 | TOACACACACACACACACACACACACACACACACACACAC | |
| Part | Protease Inhibitor 4 | Ρid | AF110e7 | S'Flank | | 8541045 | DIA V4 PA | TACAACCTTTTCCCCTCACA | 35 | TOACOTOTOTOTOTO | |
| PA AETHOS STRBM O AETHOS FRANCESCALACION TOTAL XOMPEP2 AETODOS Immuni 0 AETODOS TOTAL | Protease Inhibitor 4 | L | AF110s8 | 5'Flank | | AE110n1n2 | DIA V1 640 | ATGGTGACACCCCACTATAT | 130 | TOTTACCOCTACACACACACACACACACACACACACACAC | |
| XPWEPS AETORSA Information OF AETORSA TITTICAMAGICTUCAL COLOR ACTUAL ACT | Protease Inhibitor 4 | PIA | AF110e9 | 5'Flank | | AE110n1n0 | DIA V4 44s | ATOTOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOG | 100 | TOTTACCOCTACACACACA | |
| XPNFEP2 AE100626 Information ORGANICATION ARTHREP (ARTHREAD CONTRICATION) AR | Aminopeotidase P (membrane-bound) | XPNPEP2 | AF100c24 | introd11 | | AF100045048 | YDNDED9 V43a | TITTOAAACCTOCACACTOTAC | 80 | TOCACTTOTOCTOTTOAGG | |
| XPWEEZ AE100260 Infanit 0 AE1002890 XPNPEEZ/X88 TAMTIGACIGGOCTIG 944 CAGCICTAGGOCTITICATT XPNPEEZ AE100227 Infanit 0 AE10028940 XPNPEEZ/X814 GAGCITICAGGOCTITICATT 965 TCACAGGACCTITICATT XPNPEEZ AE100220 Infanit 0 AE10028940 XPNPEEZ/X8144 GAGCITICAGGACCT 969 ACACATACTICTAGGACCT XPNPEEZ AE100220 Exord 0 AE10029294 XPNPEEZ/X8144 GAACTICCAGACAGGACC 969 ACACATACTICTAGAGCACG XPNPEEZ AE100220 Exord 0 AE10029294 XPNPEEZ/X8144 GAACTICCAGAGAGGACC 969 ACACATACTICTAGAGGACC BDKRB1 AE100220 Exord 0 AE1002920 AVAINTAGAGAGGACC 969 ACACATACTICAGGAGATT BDKRB1 AE100220 Exord 0 AE1002920 AVAINTAGAGAGGACC 969 ACACATACTACTAGGAGATT BDKRB2 AE100220 Exord 0 AE1002920 AVAINTAGAGAGAACT 97 ACACATACTACTAGAGAACT BDKRB2 | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s25 | Infron13 | c | AF100n49n50 | XPNPEP2 X13a | TAAATGACAGGTCAGGCTTG | 963 | CAGCTCTCAGGCCTTTCATT | |
| XPNFEP2 AE100820 Intron1 0 AE1008294 XPNFEP2 X814 GGCCCATGTCATTATGAGTAC 965 TCAGGGCTACCTTTTGTCT XPNFEP2 AE100829 Emmal 0 AE100β2994 XPNFEP2 X2144 GAACTTCCAAAGTCCACC 969 ACACATACTTCTAAGCCCACG XPNFEP2 AE100829 Emmal 0 AE100B2994 XPNFEP2 X2144 GAACTTCCAAAGTCCACCCCCG 969 ACACATACTCTCAAAGCCCACG BONTBB1 AE100820 Emmal 0 AE100B2094 XPNFEP2 X2144 GAACTTCCAAAGTCCACCACG 969 TGCACTCTCACACTTCACCACCACCCACG BONTBB1 AE100810 Emmil 0 AE100B20203 UMESSI X2184 ACTTCCCAGACTCAAGGGATC 969 TGCACGTGTTAACCT BONTBB1 AE100810 Emmil 0 AE100820206 UMESSI X2184 ACTTCCCAGACTCAAGGGATC 970 CGTGGTGTTCAACTTAACCT BONTBB1 AE100810 DACCACACAGGATCAAGGGATC 971 CGTGGTGTGTAACTTAACCT BONTBB1 AE100810 AE10082020 UMESSI X2184 ACTTCCCAGACTCAAGAGATCAAGGGATC 971 CGTGGTGTGTCAACTTAACTAACTAACTAACTAACTAACT | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s26 | Infron13 | • | AE100p49p50 | XPNPEP2 X13a | TAAATGACAGGCTTG | 984 | CAGCTCTCAGGCCTTTTCATT | |
| XPNPEP2 AE100269 EDMORTORY XPNPEP2 AE100260CAGG 986 ACACATACTCTCAAGCCCAGG XPNPEP2 AE100269 EDMORTORY AE100260CAGG 987 ACACATACTCTCAAGCCCAGG XPNPEP2 AE100269 AE100260CAGG 989 ACACATACTCTCAAGCCCAGG BDKRB1 AE100260 Exor3 0 AE100260CAGG 989 TGCACCTCTCAACTCAAGGG BDKRB1 AE1002610 Exor3 0 AE100260CAGG 989 TGCACCTCTCAACTCAACTCAAGGACTCAAGGACTCAACT | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s27 | Infron7 | 0 | AE100p29p30 | XPNPEP2 X88 | GGCCCATGTCATTAATGAGTAC | 962 | TCAGGGCTACCTTTTGTCCTT | |
| XPNPEP2 AE100220 Emoit 0 AE10023994 XPNPEP2 X21144 GAACTITICCAAAGGCC 967 ACACATACTICTCAAGGCCGCG RAPNEP2 AE100240 AE100247D18 XPNPEP2 X81 GAGATITICTTCAAGGCC 988 TGGACGTCTCACTATACT BDKRB1 AE103810 Exond 0 AE1002520 U48231 X2168 ACTITCCCAGACTCCAGCTACC 970 CGTGGTGTGTCTCACTATACT BDKRB1 AE103810 Exond 0 AE10025206 U48231 X2168 ACTITCCCAGACTCCAGCTACCAGCTACTACGCATT BDKRB1 AE103812 Exond 0 AE10025206 U48231 X2168 ACTITCCCAGACTCCACAGCTACTACGCATT 970 CGTGGTGTGTTCACTACTACTACTACTACTACTACTACTACTACTACTA | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s28 | Exon21 | ° | AE100p93p94 | XPNPEP2 X21.148 | GAACTITCCAAAGTGCAGCC | 996 | ACACATACTCTCAAGCCCACG | Ĺ |
| WINEPEZ METORSON Exoné 0 AE1009JD/B XPNPEPEZ XSB GAGAMTCTTTTCCAGAGGGTC 968 TCGAGGCTCTCACCTATACCT BDKRB1 AE100810 Exond 0 AE100825269 U48231 XZBs ACTTCCCAGACTCAAGGGATC 970 CGTGGTGTTCATGCAATT BDKRB1 AE103810 Exond 0 AE103825269 U48231 XZBs ACTTCCCAGACTCAAGGGATC 970 CGTGGTGTTCATGCAATT BDKRB1 AE103812 Exond 0 AE103825269 U48231 XZBs ACTTCCCAGACTCAAGGGATC 971 CGTGGTGTTCATGCAATT BDKRB1 AE103814 Exond 0 AE103825269 U48231 XZBs ACTTCCCAACTCAAGGGATC 973 CGTGGTGTTCATGCAATT BDKRB2 AE104820 Exond 0 AE10482566 BCKRB2 XZBs ACTTCCCAACTCAAGGGATC 973 CGTGGTGTTCATGCATT BDKRB2 AE104820 BCKRB2 XXBs ACTTCCCAACTCAAGGGAATC 973 CGTGGTGTTCATGCATT BDKRB2 AE104820 BDKRB2 XXBs ACTTCCCAACATCAAGGGATC 975 GTGGTGTTTCATTCATT BDKRB2 | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s29 | Exon21 | 0 | AE100p93p94 | XPNPEP2_X21.148 | GAACTITCCAAAGTGCAGCC | 2967 | ACACATACTCTCAAGCCCACG | |
| BÜKRBI AE10810 Exon3 0 AE109255028 U48231 X218a ACTTCCCAGACTCAAGGGATC 970 CGTGGTGTTCATGCAATT BÜKRBI AE10810 Exon3 0 AE10925208 U48231 X218a ACTTCCCAGACTCAAGGGATC 971 CGTGGTGTTCATGCAATT BÜKRBI AE10812 Exon3 0 AE10925208 U48231 X218a ACTTCCCAGACTCAAGGGATC 971 CGTGGTGTTCATGCAATT BÜKRBI AE10810 Exon3 0 AE10925208 U48231 X218a ACTTCCCAGACTCAAGGATC 973 CGTGGTGTTCATGCAATT BÜKRBZ AE10820 Exon3 1 AE10820 U48231 X218a ACTTCCCAGACTCAAGGATC 973 CGTGGTGTTCATGCAATT BÜKRBZ AE10820 Exon3 1 AE1045306 BÜKRBZ X111a ACGACCACACAGGGAAACT 973 CGTGGTGTTCATGCATT BÜKRBZ AE10820 BÜKRBZ X11a ACGACCACACAGGGAAACTTCTC 975 GAGGACGTTTTGCCATT BÜKRBZ AE10820 BÜKRBZ X11a ACGACCACACAGGGAAACTTCTC 975 TTTTTGCCATTCCTTTGCATT BÜKR | Aminopeptidase P (membrane-bound) | XPNPEP2 | AE100s30 | Exon6 | 0 | AE100pJ7p18 | XPNPEP2_X58 | GAGAATCTCTTTCCAGAGGCC | 896 | TGCACGCTCTCACCTATACCT | Ĺ |
| BÜKRB1 AE10811 Exons 0 AE10925926 U48231 X2.18s ACTITOCCAGACICAAGGGATC 971 CGTGGTGTGTTCATGCAATT BÜKRB1 AE10814 Exon3 0 AE10825926 U48231 X2.18s ACTITOCCAGACICAAGGGATC 973 CGTGGTGTTGATGCAATT BÜKRB1 AE10814 Exon3 0 AE10826926 U48231 X2.18s ACTITOCCAGACICAAGGGATC 973 CGTGGTGTTCATGCAATT BÜKRB1 AE10814 Exon3 0 AE10826926 U48231 X2.18s ACTITOCCAGACICAATT 973 CGTGGTGTTCATGCAATT BÜKRB2 AE10814 Exon3 1 AE10463026 U48231 X2.18s ACTITOCCAATAACCATT 974 GGGGTGTTTGCCGGAATT BÜKRB2 AE10463026 BÜKRB2 AE10463026 BÜKRB2 X111s ACGACCACAGGGAAACTTCTC 975 GGGGTGTTTGCCGTC BÜKRB2 AE10463026 BÜKRB2 X111s ACGACCACAGGGAAACTTCTC 976 GGGGTGTTTGCCTTGTGC BÜKRB2 AE10463026 BÜKRB2 X11s ACGACCACAGGGGAAACTTCTC 976 TTTTTGTCCTTTGTGC BÜKRB2 <td>Bradykinin Receptor B1</td> <td>BDKR81</td> <td>AE103s10</td> <td>Exon3</td> <td>0</td> <td>AE103p25p26</td> <td>U48231_X2.f8a</td> <td> ACTTCCCAGACTCAAGGGATC</td> <td>969</td> <td>CGTGGTGTGTTCATGCAATT</td> <td>Ĺ</td> | Bradykinin Receptor B1 | BDKR81 | AE103s10 | Exon3 | 0 | AE103p25p26 | U48231_X2.f8a | ACTTCCCAGACTCAAGGGATC | 969 | CGTGGTGTGTTCATGCAATT | Ĺ |
| BÜKRBI AE108312 Exont 0 AE10826268 U48231 X2.18a ACTITOCCAGATICAAGGGATC 971 CGTGGGTGTTCATICAATT BÜKRBI AE108314 Exont 0 AE10826268 U48231 X2.18a ACTITOCCAGATICAAGGGATC 972 CGTGGTGTTCATICAATT BÜKRBI AE10830 Exont 1 AE10826268 U48231 X2.18a ACTITOCCAGATICAAGTAT 973 CGTGGTGTTCATICAATT BÜKRBI AE108430 Exont 1 AE1046369 BÜKRBI X11a ACGACCACAGGGAAATTTTTGCCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGGAAATTTTGCACAGAGAAATTTTACAGGAAATTTTACAGGAAATTTTACAGGAAATTTTACAGAGAGAAATTTTACAGAGAGAAATTTACAGAGAGAG | Bradydnin Receptor B1 | BOKRB1 | AE103s11 | Exon3 | 0 | AE103p25p28 | U48231_X2.f8a | ACTTCCCAGACTCAAGGGATC | 870 | CGTGGTGTGTTCATGCAATT | ۵ |
| BÜKRBZ AE103813 Exonis 0 AE10325266 U48231 XZ.NB ACTICOCAGA/CTCAAGGGAATC 972 CGTGGTGTGTTCAATGGAATT BÜKRBZ AE104830 Exonis 1 AE10453664 U48231 XZ.NB ACTICOCAGA/CTCAAGGGAATC 973 CGTGGTGTTTGGCCGTC BÜKRBZ AE104830 Exonis 1 AE10463664 BÜKRBZ AE104637 FR GGGTGATTTGGCCGTC BÜKRBZ AE104830 Immort 1 AE1046102 BÜKRBZ AE104630 | Bragyanin Hacaptor 81 | BUKHBI | AE103812 | Exor3 | ٥ | AE103p25p26 | U48231_X2.f6a | ACTTCCCAGACTCAAGGGATC | 971 | CGTGGTGTTCATGCAATT | ۵ |
| BOKHER AETONS V AETONSCIENCY STATE CGGTGGTTTTTGGCGTA BOKHER AETONS V AETONSCIENCY STATE GGGTGATTTTGGCGTA BOKHER AETONSCIENCE BOKHER XIII ACGACCATCCAATACATTTTC 975 GAGGACGTTTTTGGCGTC BOKHER AETONSCIENCE BOKHER XIII ACGACCACAGGGAAACTTCTC 977 GAGGACGTTTTTGCCGTC BOKHER AETONSCIENCE BOKHER XIII ACGACCACAGGGAAACTTCTC 977 GAGGACGTTTTGCCGTC BOKHER AETONSCIENCE BOKHER XIII ACGACCACAGGGAAACTTCTC 977 GAGGACGTTTTGCCGTC BOKHER AETONSCIENCE 977 GAGGACGTTTTGCCGTC 977 GAGGACGTTTTGCCGTC BOKHER AETONSCIENCE 978 TTTTTGCCTTCCTTTGCGTTGCCTTGGACC 979 TTTTTGTCCTTCGTTGACCTTGGACC BOKHER AETONSCIENCE 979 TTTTTGTCCTTTGGACCTTGACCTTCCTTGATGACCACGGACAACTTGACCACGACGACAACACTTGACCACGACGACAACACTTGACCACACGACGACAACACTTGACCACACGACGACAACACTTGACCACACACGACGACAACACTTCACACACA | Brachdeln Decembr Dt | DOVIDO PONCO | AE103513 | Exons | ٥ | | | ACTICCCAGACTCAAGGGATC | 972 | CGTGGTGTTCATGCAATT | 6 |
| BOKRB2 AETOHS21 Exonomic Legistration FEROHS21 Exonomic Legistration FEROHS22 FEROHS23 < | Brachdrin Resenter Ro | ROKBRO | AF10Ac20 | Exons | - | | 048231 A2.108 | ACHICCAGACHCAAGGGATC | 8/3 | CGIGGIGIICAIGCAAII | ֓֟֝֟֓֓֓֓֓֓֓֓֓֓֓֓֓֓֟֓֓֓֟֓֓֓֟֓֓֓֓֟֓֓֓֟֓֓֓ |
| BDKRB2 AETONS LEAD 1 AETONS | Brachdin Boomer 82 | BOKEE | AE404634 | STORES OF | 1 | AE 104505054 | DUNHDZ A3.IZB | GCCACCIICCAAIAAACCAII | 9/4 | GGGIGALAIGGACAGCAGAAG | - |
| BÜKRBZ AE104530 Infront 1 AE1045010 BOKRBZ AE10450 | Brachdrin Receptor R2 | BOKBR | AFIDAGO | Infrant | | AE104po 1poz | BDVODS V1646 | ACGACCACAGGGAAACH CHC | 8/2 | GAGGACGIIIIIGCCGIC | |
| BÜKRB2 AETOHSS4 Eword 1 AETOHS/35/4 BÜKRB2 73.77a TÖGTGITAL/TÖCTTCA/TÖGTC 978 BÜKRB2 AETOHSS9 Exord 1 AETOHS/35/4 BÜKRB2 X3.77a TÖGTGITAL/TÖCTTCA/TÖGTC 879 PM AETOHSS9 Exord 1 AETOHS/35/4 BÜKRB2 X3.77a TÖGTGITAL/TÖCTTCA/TÖGTC 879 PM AETOHSS9 Exord 0 AETOHS/35/4 BÜKRB2 X3.77a TÖGTGITAL/TÖCTTCA/TÖGTC 870 PM AETOHSS9 Exord 0 AETOHSS9 PH, XHs ATTOCTGG/TCA/TÖGTC 890 PM AETOHS PH, XHS ATTOCTGG/TCA/TÖGTC 882 PH PM AETOHS PH, XHS ATTOCTGG/TCA/TÖGTC 892 PM AETOHS PH, XHS AGTG/TGA/ACCCCGA/TCT/TA 893 PM AETOHS Inform AETOHS Inform AETOHS/TCA/TA 893 ACEZ AETOHS Inform 1 AETOHS/TCA/TA 896 | Bradykirin Receptor B2 | BOKRB2 | AE104833 | Intron | - | AF 104n81n82 | RDKRR9 X1 fts | ACGACCACAGGGAAACTTCTC | 0/40 | GAGGACGTTTTGCCGTC | |
| BDKRB2 AE104s36 Exord 1 AE104p73p74 BDKRB2 X3.77a TOSCTGTACTCCTTCATGGTC 979 PI4 AE110s24 Exord 0 AE110p26p30 PA AE110p26p20 PA PI4 AE110s1 Exord 0 AE110p26p30 PA AAB AGTGGTGACCTCTGGACTGTT 881 PI4 AE110s1 Exord 0 AE110p102 PI4 X111a ATGGTGACACTCTGAT 882 PH AE10s2 Flenk 0 AE110p102 PI4 X111a ATGGTGACACTCCACT 883 TACRI AE10s2 Flenk AE10p102 PI4 X111a ATGGTGACACTCCACT 883 TACRI AE10s2 Flenk AE10p102 PI4 X111a AGTGTGACACCCCACTCTAT 883 AE10s2 Flenk AE10p102 PI4 X11fa AGTGTGACACCCCACTCTAT 883 AE10s2 Flenk AE10p102 TACRI X14a AGTGACTACACACACACACTCTAT 884 ACC2 AE10sa Infrown AE10p102 AE10p102 ACCATACACACACACACACA | Bradykinin Receptor B2 | BOKRB2 | AE104834 | Exon3 | - | AF104073074 | BOKRR9 X3 77a | TOGCTGTACTCCTTCATGGTC | 978 | THITTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO | |
| BDKRB2 AE104596 Exord 1 | Bradyldnin Receptor B2 | BDKRB2 | AE104s35 | Exon3 | - | AE104p73p74 | BDKRB2 X3.f7a | | 828 | THIRETCHICCHIGIGAC | |
| P14 AE110s10 Exon4 0 AE110p28p30 P14_X4a ATTICTGGCTCTCGCAGTCTT 881 P14 AE110s1 Exon1 0 AE110p102 P14_X1f1a ATGGTGAGACCCCGACTCTAT 882 P14_X151 AE110s1 P14_X1f1a ATGGTGAGACCCCGACTCTAT 883 P14_X1f1a ATGGTGAGACCCCGACTCTAT 883 P14_X151 AE106s2 F18nk 0 AE106p101 P14_X1f1a ATGGTGAGACCCCACTCTAT 883 P14_X151 AE106s2 F18nk 1 AE106p101 F1ACR1 AGTTGCTCCACAT 884 AE106s2 Infront 1 AE106p101 TACR1 AAGTTACTCCACAT 884 ACE2 AE106s2 AE106p101 AE106p101 AE106p101 AE106p101 AE106p101 | Bradykinin Receptor B2 | BDKRB2 | AE104836 | Exori3 | | AE104p73p74 | BDKHB2_X3.f7a | TOGCTGTACTCCTTCATGGTC | 086 | TTTTGTCCTTCCTTGTGAC | |
| Pl4 AE110s11 Exont 0 AE110p1p2 Pl4 X11fa ATGGTGAGACCCGACTCTAT 882 ACED AE110s12 STRINK 0 AE110p1p2 Pl4 X1fia ATGGTGAGACCCCGACTCTAT 883 AE108s Intron | Protease Inhibitor 4 | P14 | AE110s10 | Exon4 | 0 | AE110p29p30 | PI4_X48 | ATTICTGGCTCTCGCAGTCTT | 981 | CCTTTCCAGAGGCAGAAACTT | |
| P14 AE110s12 S Fank 0 AE110p1p2 P14 X1.fis ATGGTGAGACCCGACTCTAT 883 AE110s2 Intron | Protease inhibitor 4 | Pi4 | AE110s11 | Exon1 | 0 | AE110p1p2 | PI4_X1.f18 | ATGGTGAGACCCCGACTCTAT | 883 | TGTTACCCCGTACAGACAAGG | Ĕ |
| TACR1 AE108s8 Intron 1 AE108p3p10 TACR1 Xsa AGGTTGCAGTCCCCACT 884 TACR1 AE108s9 Intron3 1 AE108p13p14 TACR1 Xsa CTGGGTTCCAAAGACACTGAA 885 ACE2 AE108s9 Intron3 1 AE109p3p30 ACE2 Xi3a CACCATAGCAGAGAAAGAAGA 886 | Protease Inhibitor 4 | P14 | AE110s12 | 5' Flank | 0 | AE110p1p2 | PI4_X1.f18 | ATGGTGAGACCCGACTCTAT | 983 | TGTTACCCCGTACAGACAAGG | |
| ACE | Tachykinin Receptor 1 | TACR1 | AE106s8 | Intron4 | - | AE108p9p10 | TACR1_X48 | AAGTTAGCTGCAGTCCCCACT | 984 | GCTTCATCCCATACTGTGCA | |
| ACEZ AELOSB INTONIS I AELOSPESSO ACEZ X138 CACCATAGCAGAGAAGCA 986 | l achykmin Receptor 1 | TACH | AE106s9 | Intron3 | - | AE106p13p14 | TACR1_X3a | CTGGGTTCCAAAGACACTGAA | 982 | TATGCAGGTGACAAGTCTCCC | |
| | Angiotensin Converting Enzyme 2 | ACE2 | AE10988 | Intron13 | - | AE109p29p30 | ACE2_X138 | CACCATAGCAGAGAAAGAAGCA | 986 | GCCAAGTCAAAGAGAAGAACC | _ |

| NO:) | Τ | | I | Ī | I | T | Ī | 1 | Ţ | T | 1 | 1 | | | Ī | Γ | Τ | T | | T | T | I | | | | | Γ | | | Γ | | <u> </u> | | | T | | Ī | I | 1 | | Ţ | | 1 | 1 | 1 | | | | | | | | | | | | | | | | | | | | Ī | Ī | Ţ | I | | | | | | | | | I | I | | 7 | 7 |
|--|----------------------------|----------------------------|----------------------------|----------------------------|----------------------------|----------------------------|-----------------------------|----------------------------|----------------------------|----------------------------|----------------------------|-----------------------------|-----------------------------|-----------------------------|----------------------------|----------------------------|---|--|----------------------------|----------------------------|----------------------------|----------------------------|---|----------------------------|----------------------|-----------------------|--------------|---|--|---------------|---------------|---------------------------------------|-------------|----------------|--|-----------------------|----------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|---------------|---------------|--------------|-----------------------|--------------|-----------------------|---------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|-------------------|------------------------|---------------------|-----------------------------------|----------------------------|--------------------------|--------------------------|---|---------------------------------|--------------------------------|------------------------|---------------|---------------|---------------|-----------------|---------------------|--------------|---|--|--|--------------|--------------|---------------------|------------------|------------------------|
| g primer (SEQ II | 260 | 188 | 2 6 | AG | 3 | 181 | 83 | 83 | 3 | 8 | 96 | 261 | 861 | 661 | 905 | Š | 8 | 2 2 | 3 3 | Š | 200 | 8 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 518 | 213 | 218 | 240 | 200 | 1 5 | 200 | 201 | 36 | 200 | 200 | 526 | 527 | 828 | 623 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 8238 | 539 | 95 | 22 | 542 | 535 | 25 | 545 | 47 | 25 | 1 | 95 | 3 | ğ | 88 | 906 | 202 | 808 | 608 | 810 | 811 | 613 | 710 | 513 | 814 | 615 | 818 |
| Reverse sequencing primer (SEQ ID NO:) | | | | | | | | | | | | | , | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| reverse seq name | | AFTOOMS | | | ŀ | AE100p28 | | ١ | AE100p40 | ļ | 1 | | AE100p52 | ļ | AF100PA | إ | ا, | ١ | | AE100060 | AE100p84 | AE100p84 | AE100p88 | AE100p88 | AE103p16 | AE10308 | AF103b20 | AF1004 | AF103m28 | AF104n38 | AF104n36 | AFIOAM | AESCAD | VE 1040 | ACTON ACTON | ACTORDED | ACCOUNT | ACTUADO | AETUADES | ACTUADED | AE 104p12 | AE104p12 | AE104p12 | AE104p24 | AE104p8 | AE104p6 | AE108p28 | AE108p20 | AE106p16 | AE106p4 | AE106p4 | AE108p4 | AE106p8 | AE105p20 | AE105o28 | AE105032 | AE105012 | AE105016 | AE105036 | AE107018 | AE107018 | AF107n18 | AE407m48 | ACAMPAN A | ACTOR DE | AETUVDEO | AE103012 | AE103p12 | AE103p12 | AE103p16 | AE104p68 | AE104p68 | AE104p82 | AF104n82 | AE104n88 | ACTOR 00 | AETOMOR | AE104p68 | AE104p68 | AE104p64 | AE104p60 |
| Reverse sequencing primer | CACIGGAAAGI | CTORAGE | COMMINION | CIGNAAIAICC | AGCTGCCTTCC | TCCCAGGTGAC | TCCCAGGTGAC | NCTCACTGCACA | CTCACTGCACA | TCCCAGGTGAC | ACTCCACACTG | ACTCCACACTG | ACTCCACACTG | AGCTGCCTTCC | AGCTOCCTOC | TOTTOGETOGE | 200000000000000000000000000000000000000 | CCI IGGGIAGA | CCI IGGGIAGA | CTGAAATATCC | STCCATAGGTCT | STCCATAGGTCT | TTCATGCCCTG | TTCATGCCCTG | TTTAATTCCGC | TGGCCTTGATG | TOCTTCTGGAG | TOAGGAGT | CATGCAATTTCT | TTOCTCOTT | TTCCCTCCCTT | TOTOGRADAAA | TOTOGRAPAAA | TOTO TOTO TOTO | TOTO CONTRACT | C GGAGAWAA | 10100000 | 31 ICGACGAGAC | TICGACGAGAC | 3 I CHACHANC | AAACAGGTGAA | AAACAGGTGAA | AAAACAGGTGAA | 3TGCTCATTGGC | TTTTBCATAGC | TGGATGAGGTTTTTGCATAGC | AGAGATGCTGT | AAATATGGAATC | AAACCTTGACTG | CTTCAGCTTCTCCTCC | AGCTTCTCCTCC | AGCTTCTCCTCC | TCTTCATCTGCT | CATCCCTGATAC | TGATGGGACTAC | AACCCTAAGCTG | AGCTGGGTAGT | ATGACCTGGAGA | TGGAGAGGTAG | ACAGGTGTCTTT | ACAGGTGTCTTT | ACAGGTGTGTTT | THUTOTOGOA | 100000000000000000000000000000000000000 | ATOTO A A CONTA | AICIGGAMGA | SCIECTEACCIC | CTGCTGACCTC | CTGCTGACCTC | TTTAATJCCGC | GCTGCTATTCAT | GCTGCTATTCAT | AAACTGATCTGA | AAACTGATCTGA | COCCATACATCT | 1111001001 | MACAIGGMAI | OCTOCTATICAT | GCTGCTATTCAT | аттестттсяв | TecctegatticttfAAtct |
| H | AGGCIGGIC | TOTOROTOR | SELCAGIGG | TGTCAGTGG | AGAGGTCAG | TAAACAAGCA | TAAACAAGCA | AAGAAGGA | AAGAAGGGA | TAMCAMBC | GCAACTCCCTACTCCA | acaactccc. | GCAACTCCC | AGAGGTCAG | Š | | 3 3 | AGCIGGGIA | AGCTGGGTA | TGTCAGTGG | TGGGACCTT | TOGGACCTT | GGTTGATGT | GGTTGATGT | TCAATGCTG | ATGAACAAA | AGGACCCAT | COATCAGATC | TRATATAT | CTTGGGATTCC | TTGGGAT | TTO04000 | OL DOVOUG | 011000000 | OCCUPATION OF THE PERSON OF TH | CONTROL I | 12000000 | CAGAAAGC | CAGAAAGCT | CAGAAAGCI | TGGAGGAAG | TGGAGGAAG | TGGAGGAAG | ACACAGTAG | TGGATGAGG | TGGATGAGG | TTACCGCAA | TGGCAGGAA | l'n٦ | ıo | GAGAGCTTC | GAGAGCTTC | AGGGTCACC | TCTGCAGTO | ACCCCAAAA | CCTGGGAGT | ATCTGTTGG | GTCCAACAA | OACCTOAGO | CCTCACCACAGAGGTG | CCTCACCAC | COTCACCAC | OF COLUMN | 200000000000000000000000000000000000000 | 010010010 | GIGLACLAC | CACTCTTGT | CACTCTTGT | САСТСТТВТ | TCAATGCTB | авттатастастаст | ааттатаст | OCCACCCAT | COCACCCAT | AGAAACCTC | Name of Contract o | GAGE ACS | Gerraracı | GeTTGTGCT | TGAGGGACAGITGCTT | Тессства |
| Forward sequencing primer (SEQ ID NO:) | R | \$2.0 | 8 | 23 | 22 | 28 | 8 | 30 | 31 | S | 33 | 3 | 38 | 5 | 3 5 | 5 6 | 8 : | 38 | 8 | 41 | 42 | 43 | 4 | 45 | 46 | 77 | 87 | | 2 | 3 | 2 | 2 2 | 3 3 | 5 | 8 8 | 8 1 | 2 | 80 | 200 | 8 | 5 | 162 | 63 | 164 | 992 | 98 | 291 | 8 | 69 | 22 | 1.6 | 221 | 173 | 74 | 175 | 178 | 1 | | | 981 | 5 | 183 | 1 | 3 3 | 5 | g | Į, | 772 | 73 | 174 | 175 | 776 | # | | | A | 08/ | 75 | 782 | 763 | 784 |
| Forward sequencing | | | | | 7 | * | | • | • | 1 | 7 | | • | | | | | | | , | • |) | | | | | | | | | | | | | | | | | | , | | , | | | | | | | | | | | | | | | | , | | | | | | | | | | | | | | | | | | | | | | | |
| forward seq name | AE100579 | AE100011 | AE100058 | AE100p59 | AE100p3 | AE100p27 | AE100p27 | AE100p39 | AE100p39 | AE100p27 | AE100p51 | AE100051 | AE100051 | AE100m3 | 47,000 | CONT. | AETUODS) | AE100p67 | AE100p67 | AE100p59 | AE100p83 | AE100p83 | AE100p87 | AE100p87 | AE103o15 | AF103m7 | AEtmonto | A E 4 CO-CO | AC409077 | AESTANDE | AESTANDE | AE10420 | ACTORDO | AETICADAS | AETOMOSS | AETORDES | AETURES | AE104p2/ | AE104p27 | AE104p27 | AE104p11 | AE104p11 | AE104p11 | AE104p23 | AE104p5 | AE10405 | AE108n25 | AE108019 | AE108015 | AE108c3 | AE10603 | AE108n3 | AE108o7 | AF105019 | AF105077 | AE106n31 | | AE105o15 | AE106n36 | AF107n15 | AE107n15 | AE407n46 | CICIONA | AETUVPIS | AE10/DIS | AE107p19 | AE103p11 | AE103p11 | AE103p11 | AE103p15 | AE104067 | AE 104067 | AF104m91 | AETOMOT | AE 404.07 | AE IONDB/ | AE 104D63 | AE104p67 | AE104p67 | AE104p63 | AE104p59 |
| uencing primer | CCTCCCTCACT | AGTTGCCACCC | MAGCACACAGA | MAGCACACAGA | GAGATCTTTGGA | CCAGGACTAAC | ACCAGGACTAAC | TTAGCAGATGC | TTAGCAGATGC | CAAAGGGAACCAGGACTAAC | TAGAGGCAGCC | TAGAGGCAGCC | TAGAGGCAGCC | PAGATOTTORA | TOTAL COMPANY | CACATO I DOM | CIGCILIANG | CAGTCTTCGGTA | CAGTCTTCGGTA | MAGCACACAGA | ACCTCTTGGCAG | CCTCTTGGCAG | CCCCAAGAGCC | CCCCAAGAGCC | CTCCTACCACT | STITOGCICATA | AACTOTTOTOTO | 200000000000000000000000000000000000000 | TOTACCTOROR | CTOTARATATOTO | CACCACTACACTO | 140040041 | ACCACI ICAN | ACCACI I CAN | IACCACITICA | IACCAC! I CAA | ACGAGICACGG | GCCICAICACA | GCCTCATCACA | GCCTCATCACA | гадататасда | rgAgtgtgcAAg | TOAGTGTGCAAG | эссттствет | 3AAACAAGTGGC | SAAACAAGTGGC | AAGATGATCCAC | GCAAGAAGGGG | CTCTCTGTTGCT | AAAATGAGTCTT | AGGAAAATGAGTCTT | AAAATGAGTCTT | TATGAAGGGAAT | CTGCAAGTATC | CTACAATCGGAT | AGCTTAGGTCTG | CACACCTTCTC | ATGAACCCACCA | TOAGGGTATCA | SPETIGETALE | GCTGCTGATAC | OCCUPATION | SCHOOL CALAC | GCCIGCIGAIAC | יבוורונאנוני | CCTTCTCACIC | GCAGAGAATATC | GCAGAGAATATC | GCAGAGAATATC | CCTCCTACCACT | COGGAGACATCA | COGGAGACATCA | тостаттоста | o Local Control | TOTOGOTOT | יוכומארוכו | GGGACAGTTTGT | CCGGAGACATCA | CCGGAGACATCA | стосмеаттет | CCTT18CTTTC |
| Forward sequencing prin | AGITOCTCC | CAGTAACATC | CACTTGTGG | САСТТВТВВ | COTCTGTCTCT | GCAAAGGGA | GCAAAGGGA | CTTTGCATCC | CTTTGCATCC | GCAAAGGGAA | AGTTGAGAGG | AGTTGAGAGG | AGTTGAGAGG | CTOTOTOTO | STOTOTO S | | AGGGIICG | CAAGGTGGA | CAAGGTGGA | CACTTGTGG/ | CAAGACTTC | CAAGACTTC | ACTGAACATA | ACTGAACATA | TCTGGGTTT | GACAGATTA | A TOTOTA A | 200000 | OLOGO POLOGO 00000000 | ADVECTOR OF | 44000400 | GCAGGCAAA | GCAGGCAAA | GCAGGCAVA | GCAGGCAAA | GAGC GAAC | ATCTICCIC | ATCTTCCTC | ATCTTCCTC | AAAGGCTTC: | AAAGGCTTC: | AAGGCTTC | CAGGTTCTA | TBGGAGTAT | TEGGAGTAT | Taraact | GAAAGAAAG/ | OCTOTOCTO | GGCTCCAGG | GGCTCCAGG | GGCTCCAGG | ATGGTTCCA | COGACTCAT | CCCAAGT | AAACCTOOA | TTCCACAT | ATACCACTO | CTCCATCAG | ACA CACA | OCTOACAGA. | ACACACAC | SOLONO COLOR | 3 | W I PO | CCCGTAGA | OCCTTCT00 | OCCTICTED | CCCTCTGG | тставатт | GGTGTTTA | GGTGTTTAK | CAGAAGCTG | S C C C C C C C C C C C C C C C C C C C | STOCK OF THE PERSON OF THE PER | ACC. LOS | CTCTGTGCT | GGTGTTTA | GGTGTTTA | AATCCTGGT | ACGTAGCAC |
| Target Name | XPNPEP2 X20a | XPNPEP2 X3a | XPNPEP2 X15a | XPNPEP2 X158 | XPNPEP2 X1a | XPNPEP2_X7& | XPNPEP2 X7a | XPNPEP2 X10a | XPNPEP2 X10a | XPNPEP2_X78 | XPNPEP2 X13a | XPNPEP2 X13a | XPNDEP2 X13s | VDAIDCD V4. | APPER AL | AFINETZ ARE | XPNPEP2 XBB | XPNPEP2 X178 | XPNPEP2 X17a | XPNPEP2 X154 | XPNPEP2 X21.f1s | XPNPEP2 X21.ffa | XPNPEP2 X21.23 | XPNPEP2 X21.22 | LARCH XO Pa | 148201 X9 He | 110001 VOILE | 1,000, 74- | 11000 VO 100 | DOLOGO VA 445 | BULLA VALVA | DUNNER ALIA | BURNEZ ALIZ | BURNEZ XI.IZ | BOKHB2 X1.12 | BOKREZ X1.72 | BUKHBZ XZ | BOKREZ X3.778 | BDKRB2 X3.77a | BOKHB2 X3.77a | BOKRB2 X3.13a | BDKHB2_X3.13a | BDKRB2 X3.13a | BDKRB2_X3.f8s | BDKRB2 X3.11 | BDKRR2 X3.11 | TACR1 X1.f1 | TACR1 X28 | TACR1 X3s | TACR1 X5/1s | TACR1 XS/18 | TACR1 XSHA | TACR1 XS12a | CINH X4s | C1NH XA | 300 | CANH Yans | CANH Yara | A NO AND A | DIKA YAS | W 1710 | , A. | N. A. | NLN AM | KLK1 X38 | ZZ ZZ | U48231 X2.f2a | 148231_X2.f2a | U48231_X2.f2% | 148231 X2.13a | BDKRR2 X3-5a | BOKRB2 X3-5a | BOKBR2 vd.3e | DONODO A SE | DUNNEZ XI-SE | BURNEZ AT-Z | BDKRB2 X1-14 | BOKRB2 X3-5a | BOKRB2 X3-54 | BOKRB2 x3-4a | BDKRB2 X3-3a |
| REVCOMP | ٥ | 0 | • | 0 | 0 | ۰ | ٥ | ٥ | 0 | 0 | 0 | 0 | ٥ | , | , | • | 0 | 7 | ٥ | 0 | 0 | | | ۰ | | , | | | • | 1 | 1 | | | | | | | - | - | - | - | - | - | • | - | _ | - | - | - | | - | - | - | | , | | , | , | , | | | | | | - | ۰ | 0 | 0 | 0 | ٥ | - | - | - | - | - | | - | - | F | - | - |
| EXON | Exon20 | mtron3 | Intron 15 | Intron15 | Intron1 | mtron7 | 7uontu | Untron10 | | Intron7 | Intron13 | E) ucupul | Phone 13 | 2 | | LLCOX S | Intron8 | Intron17 | Intron17 | 1ntron15 | Intron21 | 1 | Exon21 | Expn21 | | i com | | Sign | | 2 | | LODE | LIGOUS . | LEGILL. | | - 1 | | - 6 | Exon3 | - 1 | | | | | | S. Fark | 1 | Frond | 1 | FmmS | Ford | FmmS | Š | T T | | | | | ┸ | ┸ | | 5 | _1 | _1 | | | Exon3 | Expr3 | Exon3 | Frond | mont or Fin | Frond | 100 | | | | | Exon3 | Exon3 | Exon3 | Exon3 |
| OI ANS | AE10081 | AE10082 | AE10083 | AE10084 | AE100s5 | AE100s6 | AF100s7 | AE10068 | AE100s9 | AE100s10 | AE100s11 | AF100e12 | AE100e13 | V. 1000 | AE 100814 | AETWRID | AE100816 | AE100917 | AE100s18 | AE100s19 | AE100s20 | AE100s21 | AF100s22 | AF100s23 | AE 103e1 | 45655 | AFTON | AE ISSUE | AE IOSB | VE IUSES | VE IONS | AF IO | AFTONES | AE TOMBA | AE 10485 | AE 10486 | AE 10487 | AE10488 | AE104s9 | AE 104s to | AE104611 | AE104812 | AE104s13 | AE104814 | AE104818 | AE104817 | AE108s1 | AE106s2 | AE10843 | AF108a4 | AE106a5 | AF106m8 | AF108e7 | AF105e1 | AF105e2 | AFFORM | AFTORAL | AETOSAS | 9000 | AC10784 | 451072 | 200 | | AE10/84 | AE10/85 | AE 107s6 | AE103s6 | AE103s7 | AE103#8 | AE10349 | AF104s18 | AF 104e19 | AE104#20 | 10000 | AETOMEKI | AETOMOZZ | AE104e23 | AE104824 | AE104s25 | AE104626 | AE104s27 |
| HONC ID | (PNPEP2 | (PNPEP2 | CPNEEDS | (PNPEP2 | (PNPEP2 | (PNPEP2 | (PNPEP2 | (PNPEP2 | (PNPEP2 | XPNPEP2 | XPNPEP2 | XPNPED2 | YDNDEDS | 20107 | APRILLE | APPERA | XPNPEP2 | XPNPEP2 | XPNPEP2 | XPNPEP2 | XPNPEP2 | XPNPEP2 | XPNPEP2 | XPNPEP2 | BOXOB | 9000 | 00000 | Т | | | | S S S S S S S S S S S S S S S S S S S | | | | BOKERS | BUKKES | BOKERS | BDKRB2 | BOKER | BDKRB2 | BDKRB2 | BDKRB2 | | | | | TACR | T | TACRI | L | ı | L | П | 1 | ı | 300 | ı | | 2 | 3 | ı | 5 | 2 | 3 | XX | BDKRB1 | BDKR81 | BDKR81 | BDKR81 | RDKRR | BDKBB2 AF104419 | ankapa | X CONTRACTOR | S S S S S S S S S S S S S S S S S S S | BUKHBZ | _ | | | PDKRB2 | BOKRBZ |
| GENE_DESCRIPTION | pildase P (membrane-bound) | ptidase P (membrane-bound) | ptidase P (membrane-bound) | ptidase P (membrane-bound) | ptidase P (membrane-bound) | otidase P (membrane-bound) | ritriasa P (membrana-bound) | otidase P (membrane-bound) | otidase P (membrane-bound) | otidase P (membrane-bound) | otidase P (membrane-bound) | relitase P (membrane-brund) | relidace D (membrane bound) | Aldress P (Illestinglisher) | pricase P (memorane-pound) | pridase P (membrane-bound) | otidase P (membrane-bound) | Ammopeptidase P (membrane-bound) XPNPEP2 AE100s17 In | ptidase P (membrane-bound) | ptidase P (membrane-bound) | otidase P (membrane-bound) | otidase P (membrane-bound) | Aminosocidase P (membrane-bound) XPAPEP2 AE100s22 | caldase P (membrane-bound) | rachdonin Documer R1 | reddelnin December D4 | Ī | t | Dradykinin Heceptor B1 | Ì | İ | İ | | | | radyldnin Receptor B2 | radydnin Heceptor B2 | tracyktnin Receptor B2 | tradyktnin Receptor B2 | radytchin Receptor B2 | tradyktnin Receptor 62 | Fracykinin Receptor B2 | | | | | | Actividuin Recentor 1 | Achyldnin Recedor 1 | Tachvidnin Recentor 1 | Tachvidnin Recentor 1 | Tachvidnin Recentur 1 | Tachvidnin Bacantor 1 | C1 Esterate inhibitor | Ct Feterase inhibitor | C4 Estates inhibitor | Ct Estado Interno | C1 Esternes Intibility | C. Consider Hilliam | the free-theory and a free-theory | in 1 franchistoconsolosity | in the strain and sailed | NEI I UMIDALINI GERNARIA | ein 1 (renaupancreas/sailvary) | ein 1 (renal/pancreas/salivary) | on 1 (renal/pancress/sailvary) | Stadyldnin Receptor B1 | | | ĺ | | ľ | ľ | l | l | | 1 | | Γ | T | Bradytdnin Receptor B2 |

| GENE_DESCRIPTION HGNC_JD | | ID EXON | N REVCOMP | Target_Name | Forward sequencing primer | forward seq name | Forward sequencing primer (SEO ID NO:) | Reverse sequencing primer | reverse sec nume | Neverse sequencing primer (acuit no.) |
|--|---------------|----------------|-----------|-----------------|---------------------------|------------------|--|---------------------------|------------------|---------------------------------------|
| BDKRB2 | RB2 AE104828 | ts28 Exon3 | 1 1 | BOKRB2 X3-24 | TTGCTGAGACAGGAACAGTCC | AE104p55 | 785 | TATTGCACAACCATCTGTCCC | AETUADS | /10 |
| BDKRB2 | RB2 AE104829 | te29 Expn3 | - | BOKRB2 X3-2a | TTGCTGAGACAGGAACAGTCC | AE104p55 | 786 | TATTGCACAACCATCTGTCCC | AETOMOSO | 910 |
| Analotensin Converting Enzyme 2 ACE2 | Г | 9s1 Intron14 | - | ACE2 x14a | TTTTGAAAGAACCACATGGC | AE109p27 | 787 | AGTGGGATCTTTGGAGGAAAA | AE109p28 | 819 |
| H | t | ╀ | - | ACE2 x13a | CAGCTGTGTCACAAGTCCTCA | AE109p31 | 882 | ACATCTGGAACCCCTCAAAAG | AE109p32 | 820 |
| 1 | t | ╀ | | ACE2 x13a | CABCTGTGTCACAAGTCCTCA | AE109031 | 789 | ACATCTGGAACCCCTCAAAG | AE109p32 | 821 |
| Andreasin Convertion Enzyme 9 ACE9 | t | ╀ | - | ACE2 x3a | TCATTCATGTCCTTGCCCTTA | AE109p71 | 790 | TCTTCAGCAAATTTCCATTGTT | AE109p72 | 822 |
| - | t | - | - | ACE2 x3a | TCATTCATGTCCTTGCCCTTA | AE109p71 | 791 | TCTTCAGCAAATTTCCATTGTT | AE109p72 | 623 |
| | t | F | - | ACE2 x18a | GCACACAGGAAGACACACAA | AE108019 | 782 | octccccatercrctatc | A£109p20 | 824 |
| Andetensin Converting Enzyme 2 ACE2 | + | ٠ | | ACE2 x16a | GCACACAGGAAGAACACACAA | AE108p19 | 783 | CCTCCCCATGTCTCTCTATC | AE109p20 | 825 |
| 1 | t | ٠ | | Pl4 X2n | GATCTGGAGCGACTGTTCTG | AE110p23 | 784 | CACACTGATTACCTCTTCCGC | AE110p24 | 928 |
| ă | t | Ł | 0 | Pl4 X2a | GATCTGGAGGGACTGTTCTG | AE110p23 | 795 | CACACTGATTACCTCTTCCGC | AE110p24 | 827 |
| ā | t | ╀ | 0 | P4 X3a | CTTCAACATCCATTTGTGGG | AE110p27 | 962 | ACTITIGGATGCCTCCAGITIT | AE110p28 | 828 |
| ă | t | ╀ | 0 | P44 X3s | CTITCAACATCCATTTGTGGG | AE110p27 | 797 | ACTITIGGATGCCTCCAGTTTF | AE110p28 | 828 |
| 7 | t | ╀ | | PI4 X1 (Sa | CTACGCCATGCTTCCCTG | AE110019 | 798 | COGTGGTGTGGATTTAGCATA | AE110p20 | 630 |
| 29 | t | ╀ | | P4 X1.2a | TTGGGGGAGAACTGGAGTAT | AE110p7 | 862 | CCAACAGAGCAGGAAATGAAG | AE110p8 | 183 |
| A C | | ╀╌ | 0 | P14 X112a | TTGGGGGAGAACTGGAGTAT | AE11007 | 008 | CCAACAGAGCAGGAAATGAAG | AE110p8 | 253 |
| 4 | t | ╀ | 0 | Pi4 X1,f1a | AAAATTAGCTGGGTGTGGCT | AE110p3 | 801 | TAAGTGACCTGCCCAAAGTTG | AE110p4 | 833 |
| 2 | t | ╀ | 0 | Pt4 X1.f1a | AAAATTAGCTGGGTGTGGCT | AE110p3 | 802 | TAAGTGACCTGCCCAAAGTTG | AE110p4 | 834 |
| Aminopeoidase P (membrane-bound) XPNPEP2 | F | ₽ | | XPNPEP2 X128 | ATCTCCATCATCTTGGAGCCT | AE100p47 | 1014 | ACCCAAGAACCTGTCACTCCT | AE100p48 | 1040 |
| ۰ | - | ╀- | 13 | XPNPEP2 X13a | AGTTGAGAGGTAGAGGCAGCC | AE100551 | 1015 | GCAACTCCCTACTCCACACTG | AE100p52 | 1041 |
| 7 | | - | 13 | XPNPEP2 X13a | AGTTGAGAGGTAGAGGCAGCC | AE100551 | 1016 | GCAACTCCCTACTCCACACTG | AE100p52 | 1042 |
| | PEP2 AE100427 | ╄ | 0 | XPNPEP2 X84 | AGGITTCGCTGCTTTTAAG | AE100p31 | 1017 | CTTACCCTTCTTGGTTCCCAC | AE100p32 | 1043 |
| + | - | ╄ | 0 | XPNPEP2 X21.f4s | CAATGCTGTTAAATCCTCCCA | AE100p95 | 1018 | CTCACCCTCTTCTTCCTCC | AE100p96 | 1044 |
| ┰ | PEP2 AE100829 | ┞ | 0 | XPNPEP2 X21.44 | CAATGCTGTTAAATCCTCCCA | AE100p65 | 6101 | CTCACCCTCTTCTTCCTCC | AE100096 | 1045 |
| - | PEP2 AE100830 | ╀ | 0 | XPNPEP2 X5a | ACATCCATCAGCTAATGCCAC | AE100p19 | 0201 | GAACCTAGTCCAGGTCCCAAG | AE100p20 | 1046 |
| + | Т | ╀ | 0 | U48231 X2.f8a | CTCAGCCTCCTGTAGCTGAGA | AE103p27 | 1201 | TOGTGTGTTCATGCAATTTCT | AE103p28 | 1047 |
| BDKRB1 | Т | ┞ | 9 | U48231 X2 f8a | CTCAGCCTCCTGTAGCTGAGA | , AE103p27 | Z01 | TOGTOTOTICATGCAATTICT | AE103p28 | 1048 |
| BOKBB | 1- | L | 0 | U48231 X2.f8s | CTCAGCCTCCTGTAGCTGAGA | AE103027 | 1023 | TGGTGTGTCATGCAATTTCT | AE103p28 | 1049 |
| T | † | ╀ | 0 | U48231 X218a | CTCAGCCTCCTGTAGCTGAGA | AE103027 | 1024 | Tegreterrecarecatrici | AE103p28 | 1050 |
| Brackthin Receptor B1 BDKRB1 | ۲ | ╄ | 9 | U48231 X2.16a | CTCAGCCTCCTGTAGCTGAGA | AE103p27 | 1025 | TGGTGTGTTCATGCAATTTCT | AE103p28 | 1051 |
| | ١. | ╀ | - | BDKRB2 X3.12a | TTGCTGAGACAGGAACAGTCC | AE104p55 | 1028 | TATTBCACAACCATCTGTCCC | AE104p58 | 1052 |
| | t | ╄ | - | BDKRB2 X1.fta | CTCTGTGCTGGGACAGTTTGT | AE104p83 | 1027 | GAGCTACGCAAACATGGAAAT | AE104p84 | 1053 |
| | t | Ł | - | BDKRB2 X1.11a | Ĺ | AE104p83 | 1028 | GAGCTACGCAAACATGGAAAT | AE104p84 | 1054 |
| Practycinin Recentor R2 BDKRR2 | + | ١. | - | BOKRB2 X1.f1s | L | AE104pB3 | 1029 | GAGCTACGCAAACATGGAAAT | AE104p84 | 1055 |
| | † | Ł | | BDKRB2 X3.77a | CCCAGATCACCAAGCTGTAGA | AE104p75 | 1030 | CTTTTCCACTITCTTTCAGGG | AE104p76 | 1058 |
| Predydinin Recentor R2 RDK RR2 | 1 | ╄ | - | BDKRB2 X3.77a | CCCAGATCACCAAGCTGTAGA | AE104p75 | 1031 | CTTTTCCACTTCTTTCAGCG | AE104p78 | 1057 |
| | 1 | ╀ | - | BOKRB2 X3.77a | COCAGATCACCAAGCTGTAGA | AE104075 | 2001 | CTTTCCACTTCTTCAGCG | AE104p78 | 1058 |
| l | t | Ļ | 0 | Pi4 X4s | TCTCTTGCTGGCTTGGAGATA | AE110p31 | 1033 | CAGGGTGTGGAATGTCCAG | AE110p32 | 1059 |
| 1 | T | H | 0 | Pl4 X1,f1a | AAAATTAGCTGGGTGTGGCT | AE110p3 | 1034 | TAAGTGACCTGCCCAAAGTTG | · AE110p4 | 1080 |
| 1 | Pl4 AF110s12 | L | 0 | Pl4 X1.f1a | AAAATTAGCTGGGTGTGGCT | AE11003 | 1035 | TAAGTGACCTGCCCAAAGTTG | AE110p4 | 1061 |
| TACDA | t | ÷ | - | TACB! X4s | Tatroctorretroroacet | AF108n11 | 1036 | CTCACCTGTCTCACCCTCTTG | AE108p12 | 1062 |
| TACR | t | + | | TACP1 X3s | CETETECTECTECTATIBET | AF108b15 | 100) | GTAGCTGCCAAACCTTGACTG | AE106p16 | 1083 |
| ╀ | t | Ŧ. | 2 5 | ACE2 X13s | CARCTRICACARGICCTCA | AF109e31 | 1038 | ACATCTGGAACCCCTCAAAAG | AE109p32 | 1084 |
| | t | ╄ | | ACES YAS | TAAGGGTCACTCAAAAAGGGCA | AETOOREO | 1030 | TCTTCCTGGGCTTTTCAGATT | AE109060 | 1065 |

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| L_ | 1 |

| l | | ORCHID LEFT (SEO | | ORCHID RIGHT | | ORCHID_SNPIT (SEQ |
|----------|--------------------------------|------------------|---------------------------------|--------------|------------------------------|-------------------|
| SNP_ID | ORCHID_LEPT | | ORCHID_RIGHT | (SEQ ID NO:) | ORCHID_SNPIT | ID NO:) |
| AE100s1 | TATCATTTGTGCCCTATGACCG | 1066 | CAGGGTCAGGGAGAAGGC | 1154 | CCTCATCGATGTCNGCCTGCTGTCTCC | 1242 |
| AE100s10 | AAACTTCATCATCAGAGGTACCAAAG | 1067 | GAGGACATTTTGATTCAGACTCCTC | 1155 | GTGGTTTGCAAACCTTAGCATGCAC | 1243 |
| AE100s11 | ATAGAATGACTTCCTCCAGAGGGA | 1068 | CAGCCTAACCCTGYACTGGG | 1156 | TGGAAGCCCAGNCCCCAGAGGT | 1244 |
| AE100812 | TCCAGAGGGACTGGCCTG | 1069 | GAAGGCAGCCTAACCCTG | 1157 | AGCCCAGGCCCCAGAGGTYCTCCCA | 1245 |
| AE100s13 | ATAGAATGACTTCCTCCAGAGGGA | 1070 | GCTGAGAAGGGGAGAAATGTT | 1158 | AATGTTGAGAANGNCAGCCTAACCCTG | 1246 |
| 0814 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s15 | ACCCTCTGTCTGCTCGAG | 1071 | GATGGAGGGACAAGGGAG | 1159 | CCCGGSCTCTTCCTTCANGCNTTTCCT | 1247 |
| AE100s16 | AAAGAAGGAAGGAAAGGAA | 1072 | GTGTAGGAATAGAAGAAGGGGTTATAGG | 1160 | AGAAAAGCTTGNCTCAGGCAGATCAGC | 1248 |
| AE100s17 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100818 | AACACAGCAAGACCCCTCTCA | 1073 | GATCCCAGAGCATCTCTATGAGC | 1161 | TACCTAAATAAATAAAAGCCAG | 1249 |
| AE100s19 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s2 | ATAGAATTTGCAGGCAGGG | 1074 | GTATCTTTTGCAGTTCAACTCCCC | 1162 | GCAACAAGTCTCCTTTINCAGAACAGTC | 1250 |
| AE100s20 | TACCACAACAGGGGACTGG | 1075 | GATTCAGGTACTGGAGCTGCG | 1163 | AGACTTCACCTCTTGGCANCTTGGCTT | 1251 |
| AE100s21 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s22 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s23 | TTTGCCTAAGGACACACAAATTT | 1076 | GAGGTGGCTCAGGGACT | 1164 | CTGCATGTTGCTGAAGGA | 1252 |
| 0824 | CGCTATCTGATCTCCATCATCT | 1077 | CCGCACCTGGAGTTGGGG | 1165 | TINGAGCCTGTGGCTNCAACCAGACCT | 1253 |
| AE100s25 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s26 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s27 | ACAAGTAAGAGTTTGTTTGAGGAAAGG | 1078 | GAGCCCCAAAAAGTGTAAGTGA | 1166 | TTACCCTANGGCTGACCTNCCAGGAAC | 1254 |
| AE100s28 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s29 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s3 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s30 | TATCTTTCAGTTGGCACCA | 1079 | CAATGGACAAGAGGGG | 1167 | TCACCTGGCTCCTCACCGAGATTCC | 1255 |
| AE100s4 | TCCCTGCTGCTTCCCCGG | 1080 | AATATTTGTGCACTGATTTACCAGAATAG | 1168 | TATTTCAGNCCACTGACANGGCCTCAG | 1256 |
| AE100s5 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE100s6 | TGTGTGCATGAGTGTGGTG | 1081 | CTTTGTCATTTCCATACCTGTGAAA | 1169 | ACCTTCATAGAGGGTATAATAAAAG | 1257 |
| AE100s7 | ATCCAGTAATGGCAAAGCCAG | 1082 | GTCAGCCTTAGGGTAACAGTTTTG | 1170 | AAGAGTTTGTTTGAGGAAAGGGTTT | 1258 |
| AE100s8 | GCAAATCTCACGTCTGCTG | 1083 | CAGGTCTGGGGGCACAGTA | 1171 | GTAAAGGAGGTCTCNATNGCACAGGGG | 1259 |
| AE100s9 | AAAACTAGGAAAGACAGAAGCACAC | 1084 | TTTCAGAGGACTGGCAGGAG | 1172 | CACAGAGTAGAGAGNATTGCCACGAAA | 1260 |
| AE103s1 | AACTICTITGCCITCACIAACAGCI | 1085 | GATGAAGATATTGGAGCAAGACTTTTAG | 1173 | CCAGTAATTTATGTCTTTGTGGGCC | 1261 |
| AE103s10 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE103s11 | TGGACTTGATGAATGTTACCAAATT | 1086 | GACTCTGAGCCTCCTGCCTC | 1174 | ATCCTGAATTATCCAAGTGGGCCCT | 1262 |
| AE103s12 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE103s13 | CCACCGAGTITCTGGTAATITG | 1087 | CTTTGAATAGACAAATGGAAGTGTARTAAGA | 1175 | CAGCAGGAAACAAATAACAAGTATC | 1263 |
| AE103s14 | TGTCATAGCAGCAGGAA | 1088 | CCTGGCAGTTAGCCTAGAAAGC | 1176 | ACAAGTATCRGGTAATGNCCTCTCTTA | 1264 |
| AE103s2 | TGACAATGCTCCAGAAGCC | 1089 | CAACAGGACAAAAAGGTTCCC | 1117 | CTGGGACCTGCTGNACAGAGTGCTGCC | 1265 |
| AE10383 | ACTITICIGGGGAATIAAAACA | 1090 | ACCCCCAATCTACGGGA | 1178 | TGAACCAANANGCTTGGCTTTCTTATC | 1266 |
| AE103s4 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE10385 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE103s6 | TTCTGGGCAGAGAATATCTGGA | 1091 | CCACCAGGAAGATGCTGATG | 1179 | GAGCCCTCTCTGCCGTGTCATCAA | 1267 |
| AE103s7 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE103s8 | ATCTGAACATCACCGCCT | 1092 | GTAGTTGAAGAAGACGATCGC | 1180 | AGATCTGAACATCACCGCCTGCATC | 1268 |
| AE103s9 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE10481 | GAGAGCAATAAATGTCTGTTTTTTTGATAA | 1093 | CTCACCTGTGCTGCTTGTG | 1181 | CACTGGGCAAATCNGCNGGGCTCCCCC | 1269 |
| AE104s10 | GGTTGGGGCCTCAGGGTG | 1094 | GTGGCGGTGTGAAGCACC | 1182 | GTNGGAATGACAGGTNGAAGGGAGCCA | 1270 |
| | | | | | | |

| ORCHID_RIGHT GCCCTATGCATGGTAGATG | (SEQ ID NO:) | ORCHID SNPIT | ID NO: |
|----------------------------------|--|------------------------------|---|
| GCCCTATGCATGGTGATG | | | L |
| | 1183 | TTACAACATAACAGCNCATTGAGTCTT | 1271 |
| CGCCCTATGCATGGTGTA | 1184 | TAACAGCTCATTGAGTCTTKCACAG | 1272 |
| AAAAAAGAGGCTGTGTTTTGTCA | 1185 | GGGCAGTCATTCAGCACCAGAGCAC | 1273 |
| AAGGTGGCCCAGTATGAGC | 1186 | CCCTAGAAGAGTGTGAAAAGGAATG | 1274 |
| CAGTGATGGGGAATTCATTATCC | 1187 | ATTCCTTCACTCATNTATNAAACAAAA | 1275 |
| CATAAATGCCCCTCCAT | 1188 | TACGTTGAGCGATGAGCCCCAGGTT | 1276 |
| CATTGAGTCAGGGACTCAGCA | 1189 | ACAGGGGCTGGGGATNGCNAAATACAC | 1277 |
| CACTCTGAGTCCAAATGTTCTCTC | 1190 | GTGGTGGCACGGAGTCCTCAC | 1278 |
| CTCACCTGTGCTTGTG | 1191 | GTCAGGGAGGGCNCACCTGGGCGCGG | 1279 |
| CTCTTCCCCAGATCCACTGG | 1192 | TTTTTGNAGCCTTAAAACCCTTCCTTC | 1280 |
| CATACATCTCCGAAGAAACGG | 1193 | GCAGAAGCTGTCCTGTTTCCTGGGT | 1281 |
| N/A | N/A | N/A | N/A |
| GCAGGAGTGCAGAGCTCAG | 1194 | GAAGTGCCCAGGAGGCTGNTGACATCA | 1282 |
| N/A | N/A | N/A | N/A |
| N/A | N/A | N/A | N/A |
| GTTCTCCGTCCCTGCCCC | 1195 | CATTGCACCAAANCTGGATGGC | 1283 |
| GAAAGAAAGAACCATCTCCA | 1196 | GCTTTCNGGTGGTGNCAGTGCCCAGTC | 1284 |
| N/A | N/A | N/A | N/A |
| N/A | N/A | N/A | N/A |
| CAACCCTGCACTCCAAGC | 1197 | GAGCGAAGGCTTGGCTTGAGGTCATG | 1285 |
| N/A | N/A | N/A | N/A |
| N/A | N/A | N/A | N/A |
| N/A | N/A | N/A | N/A |
| GTTTGGGACCCCATGTTCTAT | 1198 | ACCTITITIGCTITICALTICALTICAL | 1286 |
| GTACATGTGAGGCATCWTTACGC | 1199 | GGCTCCCAATACTGATTCTGCTCCA | 1287 |
| N/A | N/A | N/A | N/A |
| CATCTTGAAGGAACTCAAAGACTCA | 1200 | ACCCACAGCACCCTGCTNGACCGTCTC | 1288 |
| CTTTGGATGAAAAGAGGAAGCA | 1201 | AGGGTTGCAGGGAGANCTGGGATGAGG | 1289 |
| CAAGAGAGGCGTCTTTGGAT | 1202 | GCTGGGATGANGYCTGGGGTGCTGCCT | 1290 |
| CAAAGAGGCCCTGCCGA | 1203 | GTTCTCTGGAGAAAAACTGTGCTG | 1291 |
| AACCCCTTACCCAGC | 1204 | CCCCTCTCCAAGTCTNTGTCCCACAA | 1292 |
| GGAGACCAAGGTTCCAGCTC | 1205 | GAAGAGGGAACTGAGGCAGGGACAG | 1293 |
| GAAGTCGTTGTGAGGGTTAAAGG | 1206 | AAGGGTGCTACGTANATNTGAGGCATC | 1294 |
| AGGTCTTCACCTGCTCTGCA | 1207 | CCCAGCGCTGGGGAAAGGAAGACA | 1295 |
| CAAACTCAGATTGTGGGAGGC | 1208 | GAGATGCGGTAGGAAGACTGTTAAG | 1296 |
| N/A | N/A | N/A | N/A |
| TTGAGTTGGTTGTCGCCAA | 1209 | AAGCTGGAANCCTCNAGGATGGGTTCA | 1297 |
| GATGCTGAATGGGGAAAAGG | 1210 | AAGCTCTACCACGCCTTCTCAG | 1298 |
| CATATACTCGCCCCATGAAGAC | 1211 | GGAACTTGTNCTNCTGGTCCCAGAGCA | 1299 |
| CACAACGAATGGTACTACGGC | 1212 | TACTGGCGAAGACAGCGGCGATGGG | 1300 |
| CATCATACATCCCCTCCAGC | 1213 | CCAGCAGGAGCCAGGACCCA | 1301 |
| CTACCACGAGCAAGTCTCTG | 1214 | CCAAGCGCAAGGTGAGCAGGGG | 1302 |
| CTGTKTGACTCAAACCAAATCACT | 1215 | AGGTCGGACCANCTTTTCCCAA | 1303 |
| TCAAAAATCTCAATTCTTCCCTATCT | 1216 | TCCCTATCTTTGCNACNCTNATGCTGT | 1304 |
| CATGGAAATTCCCTTCATCTG | 1217 | ACCCATACTGACCCTTTTNGCAAGTCC | 1305 |
| CCCACGAGGAGGCCAG | 1218 | AGAGCAGTTNGAGGTCAGGTNCAGGGA | 1306 |
| ╎┤┤┤╎╎┤┤┤┤ | GAAGTCGTTGTGAGGGGTAAAGG AGGTCTTCACCTGCTCTGCA CAAACTCCAGATTGTGGGGAA GATGCTGATTGTGGGCAA GATGCTGAATGGGGAAAGG CATATACTGAATGGGGAAAGG CATCACGAGAATGGTCGGC CATCACGAGAGTCTTG CTACCACGAGAGTCTTG CTACCACGAGAGTCTTG CTACCACGAGAGTCTTG CTACCACGAGAGTCTTG CTACAAAAATCTCAATCTTCCCTACT TCAAAAAATCTCAATCTTCCCTACTG CTGTKTGACTCAACCAATCCTT TCAAAAAATCTCAATCTTCCCTACTG CTGTKTGACTCAATCTTCCCTACTG CCTCGGGAAATTCCTTCATCTG CCTCCACGAGAGGCCAG CCCACGAGGAGGCCAG | | 1206 1207 1208 N/A 1209 1210 1211 1211 1213 1214 1215 1216 1216 |

| SNP_ID | ORCHID_LEFT | ORCHID_LEFT (SEQ ID NO:) | ORCHID_RIGHT | ORCHID_RIGHT (SEQ ID NO:) | ORCHID_SNPIT | ORCHID_SNPIT (SEQ ID NO:) |
|----------|----------------------------------|-----------------------------|-------------------------------|------------------------------|-----------------------------|------------------------------|
| AE106s8 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE106s9 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE107s1 | GTTCGTAGTCTCATTTCCAGATGATC | 1131 | ACACACAGCATGAAGTCTGTCAC | 1219 | CAAAATCCTGCCTAATGATGAGTGC | 1307 |
| AE107s2 | AGCATCGAACCAGAGAATTGTATG | . 1132 | CTTCCCTGGCCCTTTCTC | 1220 | TCCCTTGNACRCAGGAGTCCCCATCCC | 1308 |
| AE107s3 | CCTGCTGATACCATCACAGATG | 1133 | CATACAATTCTCTGGTTCGATGC | 1221 | GCTGTGAAGNTCGNGGAGTTGCCCACC | 1309 |
| AE107s4 | ATCGAACCAGAGAATTGTATGTGG | 1134 | GGGAGAAAAGGGCTGCA | 1222 | AAGGCRGGGATGGGGACTCCTG | 1310 |
| AE10785 | ACCTGGACCCACTCGGCT | 1135 | CCTTTCCCCACCTGG | 1223 | TGNGGCCACCCCAGCTGTGTCA | 1311 |
| AE107s6 | CCAGTAAATCAAATGTGCATCC | 1136 | CAGCCTCAGCCGAGTGGG | 1224 | ATGTGTCACGTTCTGCCATCACC | 1312 |
| AE10981 | AATAGCTTATCCAATAAGGAATAGGTTACTTT | 1137 | GAATTGATTATTTTGAGTGCACAGTC | 1225 | ATCTGGAACTTATAGTNTTGAAAGAA | 1313 |
| AE109s2 | GGGGTTCAGGGCCTTTT | 1138 | GCAAATTTAGCCAAGTCAAAGAGA | 1226 | GAGGGGTTCCAGANGTACNTATATTTA | 1314 |
| AE10983 | TGGGCCAAAGGAGACTAG | 1139 | GCTGAAGACCAGAACAAGAATTC | 1227 | AAGTAGACAAGGAATGGGTGTGAAA | 1315 |
| AE109s4 | GTGTTGAAACACACATATCTGCAAT | 1140 | TGGAAAGTTTGTAACCCAGATAATC | 1228 | TCATAATCACNANTNAAANTTAGTAGC | 1316 |
| AE109s5 | GTGTTCAACTGCAAATTAAAGATAATAAACA | 1141 | ACATGGCAAAGAAGTAAATTGCTG | 1229 | GAAATTTTGCTGAAGAGAATGCTAA | 1317 |
| AE109s6 | AACTCAAATCAAGATTATTCCCCTG | 1142 | GTTACCAAATACAACAATAACCAGTATT | 1230 | CACATGTAAATGACTCAGAATAATG | 1318 |
| AE109s7 | CCCTCACCCTTAGATGAAAAAA | 1143 | TITGAAACCAAGAATCTCCTTTAATTT | 1231 | TTCAGTTCTAGGAATNATATCAGACAC | 1319 |
| AE109s8 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE109s9 | AGGCTCACTCAAAAAGGCAATT | 1144 | TGCCTCCTGCTCATTTG | 1232 | CTTGGTAANAAGCCCCATNAATTCTTC | 1320 |
| AE110s1 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE110s10 | CACCTTGGACGTGAG | 1145 | ATGTGGCGATTGGTCTGG | 1233 | GGNTGGCACCGAGGNTGCAGCAGCCAC | 1321 |
| AE110s11 | CACCTCCTGCACTCTCA | 1146 | CATGGTGTCATTCAGGAATTTTG | 1234 | AACCTCNCCGGNCATGGGCTGGAAACA | 1322 |
| AE110s12 | AGATTTGGGGGAGAACTGG | 1147 | CAGTAGAACTGGTCTTTGTATTGTTACC | 1235 | TNTCTTGGACAGATGTTNATTATGAAA | 1323 |
| AE110s2 | CTGTACCTTCTTTTCATCTTCCCTT | 1148 | GCAGCATCATGGGCACCC | 1236 | CCGGACTGNTGTGTTCTCATCAACATA | 1324 |
| AE110s3 | AAGGAGGCTCTGCCCAG | 1149 | GATGCAACTCTAGCTTCTTGTAAAATT | 1237 | GATCCTGGCTTGTTCANTANTCTAATG | 1325 |
| AE110s4 | N/A | N/A | N/A | N/A | N/A | N/A |
| AE110s5 | CTTATCAACGACCACGTCAAGAA | 1150 | GATTTAGCATATACCAATGATCTGACTCT | 1238 | GAGGGAAGATTGTGGATTTGGTCAG | 1326 |
| AE110s6 | GTCAAACTAAATGGCTGAAAGTGG | 1151 | TTTCAGATGAGTTGATTTCATTAGTGC | 1239 | AGACCCTAAAATAAACTCTGAGGAT | 1327 |
| AE110s7 | AGGGTCAAACTAAATGGCTGAAA | 1152 | CACTTGTCTTTCAGATGAGTTGATTTC | 1240 | TAAACCATATAAAGCACTCCACAGA | 1328 |
| AE110s8 | AGAAACTGGAGTATCCTTTCTTGGA | 1153 | CTGTAGAGGTCAGTAGAACTGGTCTTTG | 1241 | TATGAAACGNGTACCANTTCTATCCCC | 1329 |
| AE110s9 | N/A | A/N | 4/8 | 4/N | V/N | A/N |

| GIVE_ID | 742. GBS | GBS_LEFT (SEQ ID NO:) | GBS_RIGHT | CBS_RICHT (SEQ ID NO:) |
|----------|--|--------------------------|--------------------------------------|------------------------------|
| AE100s1 | TGTAAAACGACGAGTAGTTCCTCCTCCTCCTCACT | 1330 | CAGGAAACAGCTATGACCAGAAGCTCTGGGGTCTC | 1451 |
| | TGTAAAACGACGGCCAGTGGCATTCACAGGTGATTCAGT | 1331 | CAGGAAACAGCTATGACCCACCAGGCAAGCAAATC | 1452 |
| AE100s11 | TGTAAAACGACGAGTTTCTGGGCTTTTACCCTCTCTC | 1332 | CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA | 1453 |
| AE100s12 | TGTAAAACGACGACTTTTCTGGGCTTTTACCCTCTCTC | 1333 | CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA | 1454 |
| AE100s13 | TGTAAAACGACGCCAGTCCAGGTGCAGGATTAACAGAC | 1334 | CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA | 1455 |
| AE100s14 | TGTAAAACGACGGCCAGTACTAGGAACTTGCACAGTCCG | 1335 | CAGGAAACAGCTATGACCATGCACATACCACAGAG | 1456 |
| AE100815 | AE100s15 TGTAAAACGACGGCCAGTCCTCACACCCTATCCTACACG | 1336 | CAGGAAACAGCTATGACCATGCACATACCACAGAG | 1457 |
| AE100s16 | TGTAAAACGACGCCAGTCAGTGAGATCTTGCCACTGC | 1337 | CAGGAAACAGCTATGACCCAAGCTAAGGAAAAGCC | 1458 |
| AE100s17 | TGTAAAACGACGAGTCAGGCAGACAATGATGTGATG | 1338 | CAGGAAACAGCTATGACCTGTGCTCCTCTGAAGTC | 1459 |
| AE100s18 | rgtaaaacgacggcagttatccaggtatggtggcatgt | 1339 | CAGGAAACAGCTATGACCATAGCGATGTTGTTGGA | 1460 |
| \E100s19 | AE100s19 TGTAAAACGACGACCAGTCAGAGGGAAGCACGTGATG | 1340 | CAGGAAACAGCTATGACCACTGGTTTCTGAAACCC | 1461 |
| AE100s2 | TGTAAAACGACGCCAGTTGTAAAGCCCTTTGCAGAAGT | 1341 | CAGGAAACAGCTATGACCCTTGTCAGCTACAAGCC | 1462 |
| AE100s20 | AB100s20 TGTAAAACGACGGCCAGTCTCTGAAAAGCCCCAGAGAAT | 1342 | CAGGAAACAGCTATGACCCTGTTGAAGCCACTCGA | 1463 |
| AE100s21 | TGTAAAACGACGCCAGTGAGGCTCCAGACTCTCTGTT | 1343 | CAGGAAACAGCTATGACCGGAGCAGCTGTAGCAGT | 1464 |
| AE100822 | AE100822 TGTAAAACGACGACCAGTCATTGCCTAGAAACCTTTGCA | 1344 | CAGGAAACAGCTATGACCATTGCTCTTTGGGGTT | 1465 |
| AE100823 | TGTAAAACGACGGCCAGTAGCCACAGCTACAATGCTGTT | 1345 | CAGGAAACAGCTATGACCAAAACCCAGAGGCAAGT | 1466 |
| E100824 | AE100824 TGTAAAACGACGCCAGTCTGCCGTCAACACAGAACTCT | 1346 | CAGGAAACAGCTATGACCGAACTTGTCCACGATCT | 1467 |
| AE100825 | TGTAAAACGACGGCCAGTAGAAGAACAGTTCTCCTCCGG | 1347 | CAGGAAACAGCTATGACCCCATGTGAACTCGTGAG | 1468 |
| AE100s26 | AB100s26 TGTAAAACGACGACCAGTCATGCCTTGCCTTGTACTTTC | 1348 | CAGGAAACAGCTATGACCGGCAACTCCCTACTCCA | 1469 |
| AE100s27 | TGTAAAACGACGGCCAGTATGGAACACAGAGGGGTTAGG | 1349 | CAGGAAACAGCTATGACCGTCTGCAAATCCACACT | 1470 |
| E100528 | AE100828 TGTAAAACGACGGCCAGTGGGTTGTATACCACACCCTGG | 1350 | CAGGAAACAGCTATGACCACAGCCAAATTCCTATG | 1471 |
| AE100s29 | TGTAAAACGACGACCAGTCGAGATAGGAAAGCCAGCTAG | 1351 | CAGGAAACAGCTATGACCGTTCTCCAACCTCTGGT | 1472 |
| AE100s3 | TGTAAAACGACGCCAGTCACTTGTGGAAAGCACACAGA | 1352 | CAGGAAACAGCTATGACCTGTCAGTGGCCTGAAAT | 1473 |
| AE100s30 | TGTAAAACGACGACCAGTAGGAAATTTGAGGCCATCACT | 1353 | CAGGAAACAGCTATGACCCCTCCTTCTACCAAGGT | 1474 |
| AE100s4 | TGTAAAACGACGGCCAGTAGCAGTCCAAGATCCCTTCCAT | 1354 | CAGGAAACAGCTATGACCGTTTCCTGAACACCTCT | 1475 |
| AE100s5 | TGTAAAACGACGAGTGAAAGAGCCCTCCCTCTCTC | 1355 | CAGGAAACAGCTATGACCTTGCAATGCGGTAGTCT | 1476 |
| AE100s6 | TGTAAAACGACGCCAGTCAAGGTGGACAGTCTTCGGTA | 1356 | CAGGAAACAGCTATGACCCTGCTGGCATTCCTCAC | 1477 |
| AE100s7 | TGTAAAACGACGCCAGTTCCTCATAGCAGCCCTATTGA | 1357 | CAGGAAACAGCTATGACCGGACGCCAGATACTTTC | 1478 |
| AE100s8 | TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT | 1358 | CAGGAAACAGCTATGACCCTGTTCTTCACTGCCTT | 1479 |
| AE100s9 | TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT | 1359 | CAGGAAACAGCTATGACCTGGGGAGTAGGTGTCTG | 1480 |
| AE103s1 | TGTAAAACGACGGCCAGTTCTTTTGCCTTCCTGGAATTCT | 1360 | CAGGAAACAGCTATGACCTCAATGCTGTTTTAATT | 1481 |
| AE103s10 | TGTAAAACGACGCCAGTCCCCAGATCTGAACATCAC | 1361 | CAGGAAACAGCTATGACCGACTGCTTGCACCTGGA | 1482 |
| AE103s11 | TGTAAAACGACGCCAGTGAACCAAGAAGCTTGGCTTTC | 1362 | CAGGAAACAGCTATGACCCTAAAATCTGTTTCCCTG | 1483 |
| AE103s12 | TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT | 1363 | CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA | 1484 |
| AE103s13 | TGTAAAACGACGCCAGTCAAGTGATCCTCCACTTTGGT | 1364 | CAGGAAACAGCTATGACCTGGTGTGTTCATGCAAT | 1485 |
| AE103s14 | AE103s14 TGTAAAACGACGCCAGTCCTCCACTTTGGTCTCCCATA | 1365 | CAGGAAACAGCTATGACCTGGTGTTCCTGCAAT | 1486 |
| AE103s2 | TGTAAAACGACGGCCAGTGCTGTAGTCTGCCACTTCCTG | 1366 | CAGGAAACAGCTATGACCGATATTCTCTGCCCAGA | 1487 |
| AE10383 | TGTAAAACGACGGCCAGTAGGACCAAGGTCTGGGAACT | 1367 | CAGGAAACAGCTATGACCCTGAATTCCTCTGGCCT | 1488 |
| AE103s4 | TGTAAAACGACGCCAGTGCCTGGAACACAGACCATTAA | 1368 | CAGGAAACAGCTATGACCAAGGCAGATGGATCAGA | 1489 |
| AE10385 | TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT | 1369 | CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA | 1490 |
| AE103s6 | TGTAAAACGACGCCAGTCCCTTCTGGGCAGAATATC | 1370 | CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC | 1491 |
| AE103s7 | TGTAAAACGACGCCAGTCCCTTCTGGGCAGAGAATATC | 1371 | CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC | 1492 |
| AE103s8 | TGTAAAACGACGACCAGTGCATCTTCCTGGTGGTGG | 1372 | CAGGAAACAGCTATGACCCTGTGGTCTTGCTATCC | 1493 |
| AE10389 | TGTAAAACGACGCCAGTCCCCAGATCTGAACATCAC | 1373 | CAGGAAACAGCTATGACCAGAATTCCAGGAAGGCA | 1494 |
| AE104s1 | TGTAAAACGACGGCCAGTGTGGTCTTTTAAAGGAGGCCTG | 1374 | CAGGAAACAGCTATGACCGACTTTTGCACCAACCG | 1495 |
| AE104810 | AE104s10 TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC | 1375 | CAGGAAACAGCTATGACCGTGCTACGTACATGTGA | 1496 |
| | | | | |

| 1104017 | カサナハイライナ 一中の中ももものになってなってもの中中ではなるの中ではある中のです | 1376 | CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA | 1497 |
|----------|--|------|-------------------------------------|------|
| APTOABLE | TOTAL DATE OF THE TOTAL DESCRIPTION OF THE TOTAL DATE OF THE TOTAL | 1377 | CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA | 1498 |
| | TGTAAAACGACGCCAGTCATCTACACCATGCATAGGGC | 1378 | CAGGAAACAGCTATGACCTGGAGGAAGAAAACAGG | 1499 |
| | | 1379 | CAGGAAACAGCTATGACCATTTCTAATCGGTCTTG | 1500 |
| | TGTAAAACGACGCCCAGTAATAAAAGAGGTGCTGACCCAC | 1380 | CAGGAAACAGCTATGACCCTAGAATCATAGGCGCA | 1501 |
| | | 1381 | CAGGAAACAGCTATGACCGCCACTTGTTTCATACT | 1502 |
| | TGTAAAACGACGAGTGAGGAATCCCTTTGACTCACC | 1382 | CAGGAAACAGCTATGACCGACTGAGCAATGTCTGG | 1503 |
| AE104819 | TGTAAAACGACGAGTTGGTTCCTTCAACTGTTGTCC | 1383 | CAGGAAACAGCTATGACCACAAACGTCCATTGAGT | 1504 |
| | TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG | 1384 | CAGGAAACAGCTATGACCGACTTTTGCACCAACCG | 1505 |
| AE104820 | AE104s20 TGTAAAACGACGGCCAGTAGATGTATGGCGGAGGTTTCT | 1385 | CAGGAAACAGCTATGACCGCCACCCATAAACTGAT | 1506 |
| AE104821 | TGTAAAACGACGCCAGTTTTTGGATGTAAACAGTGGGC | 1386 | CAGGAAACAGCTATGACCAATGTTTTGAAAGTCCC | 1507 |
| AE104s22 | AE104822 TGTAAAACGACGGCCAGTGGAAGCCCCATGTGAATAAAT | 1387 | CAGGAAACAGCTATGACCTTGAGCAAAACTGAGAA | 1508 |
| AE104923 | mena a a a concontraction of the contraction of the | 1388 | CAGGAAACAGCTATGACCACATGGAAATCTTCGCA | 1509 |
| AR104924 | AR104924 INCHARAAACGACGCCCAGTTCTCCATCTGAATGGGTTCTG | 1389 | CAGGAAACAGCTATGACCACGAGATGCAGAAGTTC | 1510 |
| AE104925 | APTO AS THE TRANSPORTED FOR THE PROPERTY OF TH | 1390 | CAGGAAACAGCTATGACCTAATCACACAGATCGCC | 1511 |
| AE104926 | AE104s26 Increasa ACGACGCCAGTGACCTCCTTGTCCATCAGTGA | 1391 | CAGGAAACAGCTATGACCCCAAGGACTCCAAAATC | 1512 |
| AE104927 | MCTAAAACGACGCCAGTCCCTCACAACGACTTCATGTT | 1392 | CAGGAAACAGCTATGACCTCACTGATGGACAAGGA | 1513 |
| AR104s28 | ARTO 4928 INCHARA A A CORCCO A CONTINUE CONCORDANTIGORIGIA | 1393 | CAGGAAACAGCTATGACCGGGTGATATGGACAGCA | 1514 |
| AE104s29 | TGTAAAACGACGCCAGTGGTCTCAGCACTGTGATCCTC | 1394 | CAGGAAACAGCTATGACCGTGCTACGTACATGTGA | 1515 |
| AE10483 | THETAPAACGACGCCAGTGCAGGCAAATACCACTTTCAA | 1395 | CAGGAAACAGCTATGACCTTGGATGAAAAAGAGGA | 1516 |
| AE104830 | TGTAAAACGACGACCAGTCCCAATACTGATTCTGCTCCA | 1396 | CAGGAAACAGCTATGACCGGAACTCAAAGACTCAA | 1517 |
| AE104831 | TGTAAAACGACGAGTTGGTTCCTTCAACTGTTGTCC | 1397 | CAGGAAACAGCTATGACCTTGAGTCAGGGACTCAG | 1518 |
| AE104832 | TGTAAAACGACGCCAGTCCTGACTCAATGGACGTTTGT | 1398 | CAGGAAACAGCTATGACCAATCCATATTCACACCA | 1519 |
| AE104s33 | TGTAAAACGACGCCAGTCCTGACTCAATGGACGTTTGT | 1399 | CAGGAAACAGCTATGACCAATCCATATTCACACCA | 1520 |
| AE104834 | | 1400 | CAGGAAACAGCTATGACCTATTGCACAACCATCTG | 1521 |
| AE104835 | | 1401 | CAGGAAACAGCTATGACCTATTGCACAACCATCTG | 1522 |
| AE104836 | | 1402 | CAGGAAACAGCTATGACCTCACTGATGGACAAGGA | 1523 |
| AE10484 | TGTAAAACGACGGCCAGTGAATCCCCAAAGAGATTGAGGC | 1403 | CAGGAAACAGCTATGACCACAAGCTTGGAGGAAGC | 1524 |
| AE10485 | TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC | 1404 | CAGGAAACAGCTATGACCGACATTCCACAGTTGTG | 1525 |
| AE104s6 | TGTAAAACGACGGCCAGTTGCTTTCCTCTTTTTCATCCAA | 1405 | CAGGAAACAGCTATGACCCAGCCTACAGGAAGTGG | 1526 |
| AE104s7 | TGTAAAACGACGGCCAGTGGACCCCACAAATCAATGCTT | 1406 | CAGGAAACAGCTATGACCATACCAACAGCTTCCCC | 1527 |
| AE104s8 | TGTAAAACGACGGCCAGTTGCTCCACGGAGCTATTTCTA | 1407 | CAGGAAACAGCTATGACCCAAAGACTCAAGTGGGA | 1528 |
| AE10489 | TGTAAAACGACGGCCAGTGTGGGAATGACAGGTGGAAG | 1408 | CAGGAAACAGCTATGACCGGGTGATATGGACAGCA | 1529 |
| AE105s1 | TGTAAAACGACGGCCAGTAGAGCATCCTCTCTTACCCCA | 1409 | CAGGAAACAGCTATGACCACTGTACCTGCCCGGTT | 1530 |
| AE105s2 | TGTAAAACGACGCCAGTAAGCCTGGAAGCTTAGGTCTG | 1410 | CAGGAAACAGCTATGACCTTTGATGCGGGGTAGTG | 1531 |
| AE10583 | ı | 1411 | CAGGAAACAGCTATGACCTACCCCTCTAACTTGCA | 1532 |
| AE10584 | | 1412 | CAGGAAACAGCTATGACCATCTGTTGGGAGCTGGG | 1533 |
| AE105s5 | TGTAAAACGACGGCCAGTACTACCCAGCTCCCAACAGAT | 1413 | CAGGAAACAGCTATGACCTGGATTGGTGACTCTTA | 1534 |
| AE105s6 | TGTAAAACGACGGCCAGTGGACCCAGATCTTCAGGTTTC | 7171 | CAGGAAACAGCTATGACCAACTGAGAGCTGAGGCT | 1535 |
| AE10681 | TGTAAAACGACGGCCAGTAGAGTGGCCAATCTTCCACTT | 1415 | CAGGAAACAGCTATGACCGTGGATCATCTTAGCCC | 1536 |
| AE10682 | _ | 1416 | CAGGAAACAGCTATGACCTGGCAGGAAAATATGG | 1537 |
| AE10683 | | 1417 | CAGGAAACAGCTATGACCCTGATCTACTTCCTCCC | 1538 |
| AE106s4 | | 1418 | CAGGAAACAGCTATGACCTTGCAAAAAGGGTCAGT | 1539 |
| AE10685 | | 1419 | CAGGAAACAGCTATGACCTCTGGAACCATCAGAAA | 1540 |
| AE10686 | | 1420 | CAGGAAACAGCTATGACCTCCAACTGCTCTTCACG | 1541 |
| AE106s7 | $\overline{}$ | 1421 | CAGGAAACAGCTATGACCATGAAATCCACCCGGTA | 1542 |
| AE10688 | | 1422 | CAGGAAACAGCTATGACCCTTCTTCCTCCTGCCCT | 1543 |
| AE106s9 | TGTAAAACGACGCCAGTCTTTAAGAGCAAGCGAAGTGG | 1423 | CAGGAAACAGCTATGACCCACACTATGGGCCAGTG | 1544 |
| AE10781 | TGTAAAACGACGCCAGTAATTGTATGTGGGGGGGCAGACT | 1424 | CAGGAAACAGCTATGACCGTGAAGCAGATGCCTGG | 1545 |
| | | | | |

| AE10782 | AE107s2 TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC | 1425 | CAGGAAACAGCTATGACCATTTTGAGGTCCACACA 1 | 1546 |
|----------|---|------|--|------|
| AE107s3 | TGTAAAACGACGCCAGTGCCCAGTTTGTTCATGTCAGT | 1426 | CAGGAAACAGCTATGACCGGAAATGAGACTACGAA 1 | 1547 |
| AE107s4 | AE107s4 TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC | 1427 | CAGGAAACAGCTATGACCAAGTCTGTCACCTTCTG 1. | 1548 |
| AE10785 | AE10785 TGTAAAACGACGACCAGTCCCTACCCCCAGTAAAATCAA | 1428 | CAGGAAACAGCTATGACCACCTCTCAGCCTCAGAC 1: | 1549 |
| AE10786 | AE107s6 TGTAAAACGACGACCAGTGCCGTCAGAGTGCTGTCTTAT | 1429 | CAGGAAACAGCTATGACCCTGTTTGTCTGCACCTG 1: | 1550 |
| AE109s1 | AE10981 IGTAAAACGACGACCAGTTGACGAGGAGTCAATTGAAAGGA | 1430 | CAGGAAACAGCTATGACCATGCAGACCAAAGCATC 1 | 1551 |
| AE109s2 | AE109s2 TGTAAAACGACGCCAGTCAAAGTAGTTGAGCAGTGGCC | 1431 | CAGGAAACAGCTATGACCGACCATACAACAATTGG 1 | 1552 |
| AE10983 | AE10983 TGTAAAACGACGCCAGTAAATGGCAGCTGTCACCATAG | 1432 | CAGGAAACAGCTATGACCACATGAATGTAAGGCCA 1 | 1553 |
| AE10984 | AE109s4 TGTAAAACGACGGCCAGTTCTGCAGAGAAATAAACCACTGA | 1433 | CAGGAAACAGCTATGACCTCTTCAGCAAAATTTCC 1 | 1554 |
| AE10985 | AE109s5 TGTAAAACGACGCCAGTGCATTCTTGTGGATTATCTGGG | 1434 | CAGGAAACAGCTATGACCTCGACAGTGGGGGAAACT 1 | 1555 |
| AE10986 | AE109s6 TGTAAAACGACGCCAGTTTGCCCATAGTGGTAACTTGC | 1435 | CAGGAAACAGCTATGACCCGAGTGGCTAATTTGAA 1 | 1556 |
| AE109s7 | AE109s7 TGTAAAACGACGCCAGTGCACACAGGAAGAACACACAA | 1436 | CAGGAAACAGCTATGACCCTCCCCCATGTCTCTT 1 | 1557 |
| AE10988 | AE109s8 ITGTAAAACGACGGCCAGTGTGCATGCATCTGTGTGTT | 1437 | CAGGAAACAGCTATGACCACATGAATGTAAGGCCA 1 | 1558 |
| AE10989 | AE10989 TGTAAAACGACGCCAGTTGCTTTCAAAATGCGATTTCT | 1438 | CAGGAAACAGCTATGACCCTTTCTTCCTGGGCTTTT 1 | 1559 |
| AE110s1 | AE110s1 TGTAAAACGACGCCAGTCAGGCATGTCAGGTTTTGAAT | 1439 | CAGGAAACAGCTATGACCTTGTAATCCATCCGTAG | 1560 |
| AE110s10 | AB110s10 TGTAAAACGACGCCAGTCTTGCTGTGTTATCCCCAAGA | 1440 | CAGGAAACAGCTATGACCCTCCTGCTTGGAACAGA 1 | 1561 |
| AE110s11 | AE110s11 TGTAAAACGACGCCAGTAAGAACATCTTTTTCTCCCCG | 1441 | CAGGAAACAGCTATGACCATCCACAATCTTCCCTC 1 | 1562 |
| AE110812 | AE110s12 TGTAAAACGACGGCCAGTGCAGGTCATGGAAGTGGATTA | 1442 | CAGGAAACAGCTATGACCAGCCATTTAGTTTGACC 1 | 1563 |
| AE110s2 | AE110s2 TGTAAAACGACGCCAGTGATCTGGAGCGACTGTTTCTG | 1443 | CAGGAAACAGCTATGACCTTTGCCTTGGTTAGGGA 1 | 1564 |
| AE110s3 | AE110s3 TGTAAAACGACGGCCAGTCTTTCAACATCCATTTGTGGG | 1444 | CAGGAAACAGCTATGACCTGACGACTTACTTTGGA 1 | 1565 |
| AE110s4 | AE110s4 TGTAAAACGACGGCCAGTCACAGGAAGCAACCTCTGAAG | 1445 | CAGGAAACAGCTATGACCGGAGCCAGAAATGGAGA 1 | 1566 |
| AE11085 | AB110s5 TGTAAAACGACGGCCAGTCCTTGCAAAATTCCTGAATGA | 1446 | CAGGAAACAGCTATGACCAGGGTTGCTCAACCCTA 1 | 1567 |
| AE110s6 | AE110s6 TGTAAAACGACGGCCAGTCCTTGTCTGTACGGGGTAACA | 1447 | CAGGAAACAGCTATGACCCCAACAGAGCAGGAAAT 1 | 1568 |
| AE110s7 | AE110s7 TGTAAAACGACGCCAGTAACGGGTACCAATTCTATCCC | 1448 | CAGGAAACAGCTATGACCCTAGCACATATCCCAGC 1 | 1569 |
| AE110s8 | AE110s8 TGTAAAACGACGCCAGTGATTTTGGGTGGATAGAAGCC | 1449 | CAGGAAACAGCTATGACCGGTTTACAAACCACTTT 1 | 1570 |
| AE11089 | AE110s9 ITGTAAAACGACGACCAGTGAAGGGTGCATGCCTGTAGT | 1450 | CAGGAAACAGCTATGACCTAAGTGACCTGCCCAAA | 1571 |

Table XII Sample Description

| ols | ma-like Total Total | 19 51 72 | 69 107 141 | $1 \qquad 1 \qquad 2$ | 89 159 215 |
|----------|---------------------|----------|------------|-----------------------|------------|
| Controls | a Angioedema-like | 2 | ∞ | 0 | |
| | Angioedema | 32 | 38 | _ | 70 |
| | Total | 21 | 34 | 1 | 26 |
| Cases | Angioedema-like | 10 | 22 | - | 33 |
| | Angioedema | 111 | 12 | 0 | 23 |
| | Race | Blacks | Caucasians | Other | Total |

Table XIII
Candidate Angioedema Susceptibility Genes

| Chromosome | Gene | Gene ID |
|------------|-----------------------------------|---------|
| 14 | Bradykinin B2 Receptor | BDKRB2 |
| 19 | Tissue Kallikrein | KLK1 |
| × | Aminopeptidase P (Membrane Bound) | XPNPEP2 |

Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events Table XIV

| | | | | | | | | Copies | | OR | OR | |
|---------|----------------|----------------------------|-------------|----|-------------|--------------|------|-----------|------------|-----------|-----------|-------------------|
| | | Sample or | Scores Test | | | Estimate | - | of Rare (| Odds Ratio | Lower 95% | Upper 95% | |
| Gene ID | Gene ID SNP ID | Subgroup | | DF | Probability | | A,a1 | Allele | $(OR)^2$ | CL | CL | p(a) ³ |
| RDKRB2 | BDKRB2 AE104s9 | | 7.01 | 2 | 0.0300 | Asymptotic , | A,T | - | 3.41 | 1.3238 | 8.7969 | 0.28 |
| | | | | | 0.0251 | Exact | | | 3.37 | 1.2261 | 10.2718 | |
| KI.K1 | AE107s2 | Blacks | 7.50 | 2 | 0.0062 | Asymptotic | C,T | 1 | 5.64 | 1.4211 | 22.3807 | 60.0 |
| | | | | | | Exact | | | 5.64 | 1.2422 | 34.7611 | |
| XPNPEP2 | AE10084 | XPNPEP2 AE100s4 Caucasians | 13.44 | 2 | | Exact | C,T | 2 | 14.95 | 1.9838 | +INF | 0.28 |
| | | Angioedema-like | | 7 | 0.0022 | Exact | | 7 | 10.82 | 1.3105 | +INF | 0.22 |
| | | Overall | 10.72 | 6 | 0.0047 | Asymptotic | | 2 | 11.11 | 1.2687 | 97.2709 | 0.23 |
| | | | | | | | | | | | | |

Most frequent (common) allele, least frequent (rare) allele.

of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.